

seqlist.txt  
SEQUENCE LISTING

10/533734  
JC17 Rec'd PCT/PTO 04 MAY 2005

<110> ERTL, Peter F.

<120> Vaccine

<130> PG5023

<140> Not Yet Assigned

<141> 2005-05-04

<150> PCT/EP 03/12402

<151> 2003-03-11

<150> GB 0225788.9

<151> 2002-11-05

<160> 89

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA primer

<400> 1

atcgctccatg ggtggcaagt ggt

23

<210> 2

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA primer

<400> 2

cggctactag tgcagttctt gaa

23

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA primer

<400> 3

atcgctactag tgagccagta gatc

24

<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA primer

<400> 4

cggctactag tttccttcgg gcct

24

seqlist.txt

<210> 5  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic DNA primer  
  
 <400> 5  
 gaattcgcgg ccgccatggg tggcaagtgg tcaaaaag 38  
  
 <210> 6  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic DNA primer  
  
 <400> 6  
 gaattcgcgg ccgccatggg gggttttcca gtcacacc 38  
  
 <210> 7  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic DNA primer  
  
 <400> 7  
 gaattcggat ccttattcct tcgggcctgt cggg 34  
  
 <210> 8  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic polylinker  
  
 <400> 8  
 agcttgccgc cgctagcgat atcggtacca tatgtcgacg gatcc 45  
  
 <210> 9  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic polylinker  
  
 <400> 9  
 gtaccgggtca attggcgccg gcgcgccata tgacgtcaga tctg 44  
  
 <210> 10  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 10  
 ccatggatcc gatctttttc cctctgcc 28  
  
 <210> 11  
 <211> 32

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 11  
 gttaggggtga aaagcttccg agtgagagac ac 32  
  
 <210> 12  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 12  
 gttaggggtga aaagcttccg agtgagagac ac 32  
  
 <210> 13  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 13  
 gttctccatc gcggccgcac tcttggcacg ggg 33  
  
 <210> 14  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 14  
 gaattcgcg cgcctatggc cgagcagctg tgggtcacc 39  
  
 <210> 15  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 15  
 gaattcggat cctcatctct gcacgacgcg gcgcttggcc cgggtggggg ccacg 55  
  
 <210> 16  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 16  
 gccaaagcgcc gcgtcgtgca gaga 24  
  
 <210> 17  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

seqlist.txt

<220>  
 <223> Synthetic primer

<400> 17  
 gccaaagcgcc gcgtcgtgca gagaatgggt ggcaagtggc caaaaagt 48

<210> 18  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 18  
 ggggagccga caggcccgaa ggaa 24

<210> 19  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 19  
 ggggagccga caggcccgaa ggaaatgaag gtcaaggaga ccagaaag 48

<210> 20  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 20  
 gccaaagcgcc gcgtcgtgca gagaatgggt gggtttccag tcac 44

<210> 21  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 21  
 gaattcgcgg ccgcatgggt ggggtttcca gtcacacc 38

<210> 22  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 22  
 gaattcggat cctcatctct gcacgacgcg gcgcttggcc cgggtggggg ccacg 55

<210> 23  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 23  
accaccttgt acttgtagag ctcgctccgc cagttatccc tcatgtcgcc gccgccgggc 60

<210> 24  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 24  
gaattcgagg ccgcatgga gccagtagat cctagac 37

<210> 25  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 25  
ttccttcggg cctgtcggc 19

<210> 26  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 26  
gccgacaggc ccgaaggaaa tggtgggttt tccagtcaca c 41

<210> 27  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 27  
gaattcggat ccttagcagt tcttgaagta ctccgg 36

<210> 28  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 28  
gaattcgagg ccgcaatgaa ggtcaaggag accagaaaga actaccagca tctgtg 56

<210> 29  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

seqlist.txt

<400> 29  
tctctgcacg acgcggcgct tggc 24

<210> 30  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 30  
gccaaagcgcc gcgtcgtgga gagaatgggt gcccgagctt cggtac 46

<210> 31  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 31  
gaattcggat ccttagcagt tcttgaagta ctccgg 36

<210> 32  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 32  
gccaaagcgcc gcgtcgtgga gagaatgggt gcccgagctt cggtac 46

<210> 33  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 33  
caacactctg gctttgtgtc c 21

<210> 34  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 34  
ggacacaaag ccagagtgtt gatgggcaag tgggtcaaaaa gtag 44

<210> 35  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 35

	seqlist.txt	
gaattcggat ccttagcagt tcttgaagta ctccgg		36
<210> 36		
<211> 44		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic primer		
<400> 36		
ggacacaaag ccagagtgtt gatgggcaag tgggtcaaaaa gtag		44
<210> 37		
<211> 38		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic primer		
<400> 37		
gaattcgcgg ccgccatggg tggcaagtgg tcaaaaag		38
<210> 38		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic primer		
<400> 38		
gccaataaag gagagaacac cagc		24
<210> 39		
<211> 49		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic primer		
<400> 39		
gccaataaag gagagaacac cagcgcctta caccctgtga gcctgcatg		49
<210> 40		
<211> 49		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic primer		
<400> 40		
gccaataaag gagagaacac cagcttgga caccctgtga gcctgcatg		49
<210> 41		
<211> 49		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Synthetic primer		
<400> 41		
gccaataaag gagagaacac cagcgccgca caccctgtga gcctgcatg		49

seqlist.txt

<210> 42  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 42  
 ggggagccga caggcccgaa ggaa 24  
  
 <210> 43  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 43  
 gaattcgcgg ccgccatggc cgagcagctg tgggtcacc 39  
  
 <210> 44  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 44  
 gccaaagcgcc gcgtcgtgca gaga 24  
  
 <210> 45  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 45  
 gccaaagcgcc gcgtcgtgca gagaatgggc cccatcagtc ccatc 45  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 46  
 cgtcacgatg ttcacctcca ggcc 24  
  
 <210> 47  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 47  
 gtggcccagag agctgcatcc g 21  
  
 <210> 48  
 <211> 48



seqlist.txt

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic primer

<400> 48  
ggacacaaag ccagagtgtt gatggccgag cagctgtggg tcaccgtc

48

<210> 49  
<211> 514  
<212> PRT  
<213> HIV-1

<400> 49  
Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln His Leu Trp Arg Trp  
1 5 10 15  
Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Gln  
20 25 30  
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr  
35 40 45  
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val  
50 55 60  
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro  
65 70 75 80  
Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys  
85 90 95  
Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp  
100 105 110  
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu  
115 120 125  
Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Thr Ser Asn  
130 135 140  
Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe  
145 150 155 160  
Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu  
165 170 175  
Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr  
180 185 190  
Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser  
195 200 205  
Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile  
210 215 220  
His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys  
225 230 235 240  
Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys  
245 250 255  
Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly  
260 265 270  
Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp  
275 280 285  
Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn  
290 295 300  
Cys Thr Arg Pro Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro  
305 310 315 320  
Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln  
325 330 335  
Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln  
340 345 350  
Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe  
355 360 365  
Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn  
370 375 380  
Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser  
385 390 395 400  
Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile  
405 410 415  
Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val

seqlist.txt

			420					425				430					
Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	Ile	Arg	Cys	Ser		
		435					440					445					
Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Thr	Glu	Gly		
	450					455					460						
Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp		
465					470					475					480		
Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys		
			485						490					495			
Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	Arg	Arg	Val	Val		
		500						505					510				
Gln	Arg																

<210> 50  
 <211> 1545  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimised DNA for gp120

<400> 50

atgaagggtca	aggagaccag	aaagaactac	cagcatctgt	ggcgctgggg	caccatgctc	60
ctgggaatgc	tgatgatctg	ctccgccgcc	gagcagctgt	gggtcaccgt	ctactacggc	120
gtgcctgtgt	ggaaggaggc	cacgaccacc	ctcttctgcg	cgagcgacgc	caaggcctac	180
gacacggaag	tgcataacgt	gtgggcgacg	catgcttgcg	tgcctacgga	ccccaacccc	240
caggaggtgg	tgctgggaaa	cgtgaccgag	tacttcaaca	tgtggaagaa	taacatggtg	300
gatcagatgc	acgaggacat	catctctctg	tgggaccagt	ccctgaagcc	ctgctgaag	360
ctgacgcctc	tctgctgac	actggactgt	gacgacgtca	acaccaccaa	cagcactacc	420
accaccagca	acggctggac	cggagagatt	cgaagggcg	agatcaagaa	ctgctccttc	480
aatatcacga	cctcgatcag	agacaagggt	cagaagggaat	acgcgctgtt	ttataatctc	540
gatgtgggtcc	ccatcgacga	cgacaatgcc	accaccaaga	acaagacgac	gcgtaatttc	600
agactcattc	actgcaacag	cagcgtcatg	acgcaggcct	gccccaaagg	gtccttcgaa	660
ccaatcccga	tccattactg	tgcccctgcc	ggattcgcga	tcctcaagtg	taacaacaag	720
accttcgacg	ggaagggcct	gtgcaccaac	gtcagcacgg	tgcagtgcac	ccatggcatc	780
cgccccgtcg	tgagcaccca	gctgctgctg	aacgggtccc	tggctgagga	ggaggtggtg	840
atccgggtcgg	acaacttcat	ggacaacacc	aagacaatca	tcgtccagct	gaacgagtct	900
gtggcgatta	actgtacccg	gcctaacaac	aacacccgta	agggcatcca	catcgggcct	960
ggacgggcct	tctatgccgc	ccgcaagatc	atcggcgaca	tccggcaggc	ccattgcaac	1020
ctctcccgcg	cccagtggaa	taacaccctg	aagcagatcg	tgatcaagct	gagagagcac	1080
tttggaataa	agaccatcaa	gttcaatcag	agttctggcg	gagaccccga	gatcgtgcgg	1140
cactccttca	actgcggggg	cgagttcttc	tactgcgata	cgacacagct	cttcaactcc	1200
acctggaacg	gcaccgaggg	caacaacaca	gagggaaact	ccactatcac	cctcccttgc	1260
cgcatacagc	agatcatcaa	catgtggcag	gaggtgggaa	aggccatgta	tgcccccccc	1320
atcggggggc	agatccgctg	ctcctccaac	atcaccggcc	tgctgctcac	cagagacggg	1380
ggcaccgagg	gcaacggcac	ggagaacgag	acggagatct	tcaggcccgg	cggcggcgac	1440
atgagggata	actggcggag	cgagctgtac	aagtacaagg	tggtgaagg	ggagccgctc	1500
ggcgtggccc	ccacccgggc	caagcgccgc	gtcgtgcaga	gatga		1545

<210> 51  
 <211> 882  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 Nef-Tatm fusion

<400> 51

atgggtggca	agtgggtcaaa	aagtagtgtg	gttggatggc	ctactgtaag	ggaaagaatg	60
agacgagctg	agccagcagc	agatgggggtg	ggagcagcat	ctcgagacct	ggaaaaacat	120
ggagcaatca	caagtagcaa	tacagcagct	accaatgctg	cttgtgcctg	gctagaagca	180
caagaggagg	aggaggtggg	ttttccagtc	acacctcagg	tacctttaag	accaatgact	240
tacaaggcag	ctgtagatct	tagccacttt	ttaaaagaaa	aggggggact	ggaagggtta	300
attcactccc	aacgaagaca	agatatcctt	gatctgtgga	tctaccacac	acaaggctac	360
ttccctgatt	ggcagaacta	cacaccaggg	ccaggggtca	gatatccact	gacctttgga	420
tggtgctaca	agctagtacc	agttgagcca	gataaggtag	aagaggccaa	taaaggagag	480

seqlist.txt

```

aacaccagct tgttacaccc tgtgagcctg catggaatgg atgaccctga gagagaagtg 540
ttagagtggg ggtttgacag ccgcctagca tttcatcacg tggcccgaga gctgcatccg 600
gagtacttca agaactgcac tagtgagcca gtagatccta gactagagcc ctggaagcat 660
ccaggaagtc agcctaaaac tgcttgtacc aattgctatt gtaaaaagtg ttgctttcat 720
tgccaagttt gtttcataac agctgcctta ggcattctct atggcaggaa gaagcggaga 780
cagcgacgaa gacctcctca aggcagtcag actcatcaag tttctctatc aaagcaaccc 840
acctcccaat ccaaagggga gccgacaggc ccgaaggaat aa 882

```

<210> 52  
 <211> 293  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 Nef-Tatm fusion

<400> 52  
 Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val  
 1 5 10 15  
 Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala  
 20 25 30  
 Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr  
 35 40 45  
 Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu  
 50 55 60  
 Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr  
 65 70 75 80  
 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly  
 85 90 95  
 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu  
 100 105 110  
 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr  
 115 120 125  
 Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys  
 130 135 140  
 Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu  
 145 150 155 160  
 Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro  
 165 170 175  
 Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His  
 180 185 190  
 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser  
 195 200 205  
 Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln  
 210 215 220  
 Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His  
 225 230 235 240  
 Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg  
 245 250 255  
 Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His  
 260 265 270  
 Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro  
 275 280 285  
 Thr Gly Pro Lys Glu  
 290

<210> 53  
 <211> 690  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 trNef-Tatm fusion

<400> 53  
 atgggtgggtt ttccagtcac acctcaggta cctttaagac caatgactta caaggcagct 60  
 gtagatctta gccacttttt aaaagaaaag gggggactgg aagggctaata tcactcccaa 120

## seqlist.txt

```

cgaagacaag atataccttga tctgtggatc taccacacac aaggctactt ccctgattgg 180
cagaactaca caccagggcc aggggtcaga tatccactga cttttggatg gtgctacaag 240
ctagtaccag ttgagccaga taaggtagaa gaggccaata aaggagagaa caccagcttg 300
ttacaccctg tgagcctgca tggaatggat gaccctgaga gagaagtgtt agagtggagg 360
tttgacagcc gcctagcatt tcatcacgtg gcccagagagc tgcattccgga gtacttcaag 420
aactgcacta gtgagccagt agatcctaga ctagagccct ggaagcatcc aggaagtcag 480
cctaaaactg cttgtaccaa ttgctattgt aaaaagtgtt gctttcattg ccaagtttgt 540
ttcataacag ctgccttagg catctcctat ggcaggaaga agcggagaca gcgacgaaga 600
cctcctcaag gcagtcagac tcatcaagtt tctctatcaa agcaaccac ctcccaatcc 660
aaaggggagc cgacaggccc gaaggaataa 690

```

<210> 54  
 <211> 229  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 trNef-Tatm fusion

```

<400> 54
Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
1      5      10      15
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
20      25      30
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
35      40      45
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
50      55      60
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
65      70      75      80
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
85      90      95
Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
100     105     110
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
115     120     125
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
130     135     140
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
145     150     155     160
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
165     170     175
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
180     185     190
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
195     200     205
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
210     215     220
Thr Gly Pro Lys Glu
225

```

<210> 55  
 <211> 1461  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c

```

<400> 55
atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60
accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgca taactgtgtg 120
gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420

```

seqlist.txt

```

aaggtgcaga aggaataacgc gctgtttttat aatctcgaatg tgggtcccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcattccgcc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcccga gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ctttcaactg cgggggagc 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacgc ggggcccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaaggtggt gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagatg a 1461

```

<210> 56  
 <211> 486  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c

<400> 56

Met	Ala	Glu	Gln	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp
1				5					10					15	
Lys	Glu	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr
			20					25					30		
Asp	Thr	Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr
		35					40					45			
Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Tyr	Phe
	50					55					60				
Asn	Met	Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile
65				70					75					80	
Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu
			85					90						95	
Cys	Val	Thr	Leu	Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Asn	Ser	Thr	Thr
			100					105					110		
Thr	Thr	Ser	Asn	Gly	Trp	Thr	Gly	Glu	Ile	Arg	Lys	Gly	Glu	Ile	Lys
		115					120					125			
Asn	Cys	Ser	Phe	Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys
	130					135					140				
Glu	Tyr	Ala	Leu	Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp
145				150					155					160	
Asn	Ala	Thr	Thr	Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His
				165					170					175	
Cys	Asn	Ser	Ser	Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu
			180					185					190		
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys
		195					200					205			
Cys	Asn	Asn	Lys	Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser
	210					215					220				
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu
225				230					235					240	
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp
			245					250						255	
Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser
			260					265					270		
Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile
		275					280					285			
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
	290					295					300				
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
305				310					315					320	



seqlist.txt

Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
			325						330					335	
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
				405					410					415	
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly
			420					425					430		
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465					470					475					480
Arg	Arg	Val	Val	Gln	Arg										
				485											

<210> 57  
 <211> 2340  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c'

<400> 57

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaa	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatg	cttgcgtgcc	tacggacccc	aacccccagg	agggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtccct	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaataacg	gctgttttat	aatctcgatg	tggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tcgcatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	cacccagctg	720
ctgctgaacg	gggtccctggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtctgtgg	cgattaactg	tacccggcct	840
aacaacaaca	cccgttaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgccc	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggagc	1080
ttcttttact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggaac	1140
aacacagagg	gaaactccac	tatcacccct	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	cccccatcg	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcagcgag	1320
aacgagacgg	agatcttcag	gcccggcggc	ggcgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaagggtgg	gaagggtggag	ccgctcggcg	tggtccccc	ccgggccaag	1440
cgccgcgtcg	tgagagaga	gggtggcaag	tggtcaaaaa	gtagtgtggt	tggtatggcct	1500
actgtaaggg	aaagaatgag	acgagctgag	ccagcagcag	atggggtggg	agcagcatct	1560
cgagacctgg	aaaaacatgg	agcaatcaca	agtagcaata	cagcagctac	caatgctgct	1620
tgtgcctggc	tagaagcaca	agaggaggag	gaggtgggtt	ttccagtcac	acctcaggta	1680
cctttaagac	caatgactta	caaggcagct	gtagatctta	gccacttttt	aaaagaaaag	1740
gggggactgg	aagggtctaat	tcactcccaa	cgaagacaag	atatccttga	tctgtggatc	1800
taccacacac	aaggctactt	ccctgattgg	cagaactaca	caccagggcc	aggggtcaga	1860
tatccactga	cctttggatg	gtgctacaag	ctagtaccag	ttgagccaga	taaggtagaa	1920
gaggccaata	aaggagagaa	caccagcttg	ttacaccctg	tgagcctgca	tggaatggat	1980
gaccctgaga	gagaagtgtt	agagtggagg	tttgacagcc	gcctagcatt	tcatcacgtg	2040
gcccagagagc	tgcatccgga	gtacttcaag	aactgcacta	gtgagccagt	agatcctaga	2100

seqlist.txt

ctagagccct ggaagcatcc aggaagtcag cctaaaactg cttgtaccaa ttgctattgt 2160  
 aaaaagtgtt gctttcattg ccaagttttgt ttcataacag ctgccttagg catctcctat 2220  
 ggcaggaaga agcggagaca gcgacgaaga cctcctcaag gcagtcagac tcatcaagtt 2280  
 tctctatcaa agcaaccac ctcccaatcc aaaggggagc cgacaggccc gaaggaataa 2340

<210> 58  
 <211> 779  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c'

<400> 58  
 Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp  
 1 5 10 15  
 Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr  
 20 25 30  
 Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr  
 35 40 45  
 Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe  
 50 55 60  
 Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile  
 65 70 75 80  
 Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu  
 85 90 95  
 Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr  
 100 105 110  
 Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys  
 115 120 125  
 Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys  
 130 135 140  
 Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp  
 145 150 155 160  
 Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His  
 165 170 175  
 Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu  
 180 185 190  
 Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys  
 195 200 205  
 Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser  
 210 215 220  
 Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu  
 225 230 235 240  
 Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp  
 245 250 255  
 Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser  
 260 265 270  
 Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile  
 275 280 285  
 His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly  
 290 295 300  
 Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn  
 305 310 315 320  
 Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys  
 325 330 335  
 Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg  
 340 345 350  
 His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln  
 355 360 365  
 Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly  
 370 375 380  
 Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met  
 385 390 395 400  
 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln  
 405 410 415  
 Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly

## seqlist.txt

										420				425				430		
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro					
										435		440		445						
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr					
										450		455		460						
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys					
										465		470		475						
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val					
										485		490		495						
Val	Gly	Trp	Pro	Thr	Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala					
										500		505		510						
Ala	Asp	Gly	Val	Gly	Ala	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala					
										515		520		525						
Ile	Thr	Ser	Ser	Asn	Thr	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu					
										530		535		540						
Glu	Ala	Gln	Glu	Glu	Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val					
										545		550		555						
Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe					
										565		570		575						
Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg					
										580		585		590						
Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro					
										595		600		605						
Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr					
										610		615		620						
Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu					
										625		630		635						
Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu					
										645		650		655						
His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp					
										660		665		670						
Ser	Arg	Leu	Ala	Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr					
										675		680		685						
Phe	Lys	Asn	Cys	Thr	Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp					
										690		695		700						
Lys	His	Pro	Gly	Ser	Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys					
										705		710		715						
Lys	Lys	Cys	Cys	Phe	His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu					
										725		730		735						
Gly	Ile	Ser	Tyr	Gly	Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro					
										740		745		750						
Gln	Gly	Ser	Gln	Thr	His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser					
										755		760		765						
Gln	Ser	Lys	Gly	Glu	Pro	Thr	Gly	Pro	Lys	Glu										
										770		775								

&lt;210&gt; 59

&lt;211&gt; 2148

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 ds-gp120c Nef-Tatm fusion

&lt;400&gt; 59

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaaag	gcctacgaca	cggaagtgca	taacgtgtgg	120
gcgacgcatg	cttgcggtgcc	tacggacccc	aacccccagg	aggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtcctt	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgatg	tggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgccggat	tcgcgatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	caccagctg	720



seqlist.txt

```

ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggctcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgccca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ctttcaactg cgggggagc 1080
ttcttttact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacatc ggggcccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtggg gaagggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgctc tgcagagaat ggtgggtttt ccagtcacac ctcaggtacc tttaagacca 1500
atgacttaca aggcagctgt agatcttagc cactttttta aagaaaaggg gggactggaa 1560
gggctaattc actcccaacg aagacaagat atccttgatc tgtggatcta ccacacacaa 1620
ggctacttcc ctgattggca gaactacaca ccagggccag gggtcagata tccactgacc 1680
tttgatgggt gctacaagct agtaccagtt gagccagata aggtagaaga ggccaataaa 1740
ggagagaaca ccagcttggt acaccctgtg agcctgcatg gaatggatga ccctgagaga 1800
gaagtgttag agtggagggt tgacagccgc ctacgatttc atcacgtggc ccgagagctg 1860
catccggagt acttcaagaa ctgcactagt gagccagtag atcctagact agagccctgg 1920
aagcatccag gaagtcagcc taaaactgct tgtaccaatt gctattgtaa aaagtgttgc 1980
tttcattgcc aagtttggtt cataacagct gccttaggca tctcctatgg caggaagaag 2040
cggagacagc gacgaagacc tcctcaaggc agtcagactc atcaagtttc tctatcaaag 2100
caaccacct cccaatccaa aggggagccg acaggcccga aggaataa 2148

```

<210> 60

<211> 715

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c Nef-Tatm fusion

<400> 60

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
      20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
      35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
      50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
      65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
      85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
      100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
      115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
      130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
      145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
      165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
      180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
      195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
      210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
      225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
      245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
      260      265      270

```

seqlist.txt

Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile
		275					280					285			
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
	290					295					300				
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
305					310					315					320
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
			325						330					335	
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
				405					410					415	
Ile	Arg	Cys	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	
			420				425					430			
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465					470					475					480
Arg	Arg	Val	Val	Gln	Arg	Met	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val
				485					490					495	
Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe
			500					505					510		
Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg
		515					520					525			
Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro
	530					535					540				
Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr
545					550					555					560
Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu
				565					570					575	
Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu
			580					585				590			
His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp
		595					600					605			
Ser	Arg	Leu	Ala	Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr
	610					615					620				
Phe	Lys	Asn	Cys	Thr	Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp
625					630					635					640
Lys	His	Pro	Gly	Ser	Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys
				645					650					655	
Lys	Lys	Cys	Cys	Phe	His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu
			660					665					670		
Gly	Ile	Ser	Tyr	Gly	Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro
		675					680					685			
Gln	Gly	Ser	Gln	Thr	His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser
	690					695					700				
Gln	Ser	Lys	Gly	Glu	Pro	Thr	Gly	Pro	Lys	Glu					
705					710					715					

<210> 61

<211> 1887

<212> DNA

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c trNef fusion

<400> 61

atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60

seqlist.txt

```

accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgca taacgtgtgg 120
gcgacgcatg cttgctgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtccct gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgtat tggtcccatc cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacgggtgca gtgcacccat ggcacccgcc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact cttcaactg cggggcgag 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcaccctc cttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacg gggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgg gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagaaat ggtgggtttt ccagtcacac ctacaggtacc ttaagacca 1500
atgacttaca aggcagctgt agatcttagc cactttttta aagaaaagg gggactggaa 1560
gggctaattc actcccaacg aagacaagat atccttgatc tgtggatcta ccacacacaa 1620
ggctacttcc ctgattggca gaactacaca ccagggccag gggtcagata tccactgacc 1680
tttgatgggt gctacaagct agtaccagtt gagccagata aggtagaaga ggccaataaa 1740
ggagagaaca ccagcttggt acaccctgtg agcctgcatg gaatggatga ccctgagaga 1800
gaagtgttag agtggaggtt tgacagccgc ctagcatttc atcacgtggc ccgagagctg 1860
catccggagt acttcaagaa ctgctaa 1887

```

<210> 62

<211> 628

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c trNef fusion

<400> 62

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser

```

## seqlist.txt

210	Thr	Val	Gln	Cys	Thr	His	215	Gly	Ile	Arg	Pro	Val	220	Val	Ser	Thr	Gln	Leu
225	Leu	Leu	Asn	Gly	Ser	230	Leu	Ala	Glu	Glu	Glu	235	Val	Val	Ile	Arg	Ser	240
					245		Thr	Lys	Thr	Ile	Ile	250	Val	Gln	Leu	Asn	Glu	255
	Asn	Phe	Met	Asp	260		Thr	Lys	Thr	Ile	Ile	265	Val	Gln	Leu	Asn	Glu	270
	Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	280	Thr	Arg	Lys	Gly	Ile	
	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	285	Arg	Lys	Ile	Ile	Gly	
	290						295					300						
	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	315	Ala	Gln	Trp	Asn	Asn	320
305	Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	330	His	Phe	Gly	Asn	Lys	
					325							335						
	Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	345	Pro	Glu	Ile	Val	Arg	
				340								350						
	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	360	Cys	Asp	Thr	Thr	Gln	
				355								365						
	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	380	Asn	Thr	Glu	Gly		
	370						375					385						
	Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	395	Gln	Ile	Ile	Asn	Met	
385						390						400						
	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	410	Pro	Ile	Gly	Gly	Gln	
					405							415						
	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	425	Leu	Leu	Thr	Arg	Asp	Gly
					420							430						
	Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	440	Glu	Ile	Phe	Arg	Pro	
												445						
	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	460	Glu	Leu	Tyr	Lys	Tyr	
	450						455					465						
	Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	475	Pro	Thr	Arg	Ala	Lys	
465						470						480						
	Arg	Arg	Val	Val	Gln	Arg	Met	Val	Gly	Phe	Pro	490	Val	Thr	Pro	Gln	Val	
					485							495						
	Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala	Ala	Val	505	Asp	Leu	Ser	His	Phe	
				500								510						
	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	Leu	Ile	520	His	Ser	Gln	Arg	Arg	
												525						
	Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr	His	Thr	540	Gln	Gly	Tyr	Phe	Pro	
	530						535					545						
	Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro	Gly	Val	555	Arg	Tyr	Pro	Leu	Thr	
545						550						560						
	Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro	Val	Glu	570	Pro	Asp	Lys	Val	Glu	
					565							575						
	Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser	Leu	Leu	585	His	Pro	Val	Ser	Leu	
					580							590						
	His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu	Val	Leu	600	Glu	Trp	Arg	Phe	Asp	
					595							605						
	Ser	Arg	Leu	Ala	Phe	His	His	Val	Ala	Arg	Glu	620	Leu	His	Pro	Glu	Tyr	
	610						615					625						
	Phe	Lys	Asn	Cys														
625																		

<210> 63  
 <211> 1517  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 Nef p17/24 fusion

<400> 63  
 tgggtgccccg agcttcggtg ctgtctggtg gagagctgga cagatgggag aaaattaggc 60  
 tgcgccccggg aggcaaaaag aaatacaagc tcaagcatat cgtgtgggccc tcgagggagc 120  
 ttgaacggtt tgccgtgaac ccaggcctgc tggaacatc tgagggatgt cgccagatcc 180  
 tggggcaatt gcagccatcc ctccagaccg ggagtgaaga gctgagggtcc ttgtataaca 240



seqlist.txt

cagtggctac	cctctactgc	gtacaccaga	ggatcgagat	taaggatacc	aaggaggcct	300
tggacaaaat	tgaggaggag	caaaacaaga	gcaagaagaa	ggcccagcag	gcagctgctg	360
acactgggca	tagcaaccag	gtatcacaga	actatcctat	tgtccaaaac	attcagggcc	420
agatgggtca	tcaggccatc	agcccccgga	cgctcaatgc	ctgggtgaag	gttgtcgaag	480
agaaggcctt	ttctcctgag	gttatcccca	tgttctccgc	tttgagtgaag	ggggccactc	540
ctcaggacct	caatacaatg	cttaataaccg	tgggcggcca	tcaggccgcc	atgcaaagtgt	600
tgaaggagac	tatcaacgag	gaggcagccg	agtgggacag	agtgcacccc	gtccacgctg	660
gccaatcgc	gcccggacag	atgcgggagc	ctcgcggctc	tgacattgcc	ggcaccacct	720
ctacactgca	agagcaaadc	ggatggatga	ccaacaatcc	tcccatccca	gttggagaaa	780
tctataaacg	gtggatcatt	ctcgggtctca	ataaaaattgt	tagaatgtac	tctccgacat	840
ccatccttga	cattagacag	ggacccaaag	agccttttag	ggattacgtc	gaccggtttt	900
ataagaccct	gcgagcagag	caggcctctc	aggaggtcaa	aaactggatg	acggagacac	960
tcctgggtaca	gaacgctaac	cccgaactga	aaacaatctt	gaaggcacta	ggcccggctg	1020
ccaccctgga	agagatgatg	accgcctgtc	agggagtagg	cggacccgga	cacaaagcca	1080
gagtgttgat	gggtgggtttt	ccagtcacac	ctcagggtacc	tttaagacca	atgacttaca	1140
aggcagctgt	agatccttagc	cacttttttaa	aagaaaaggg	gggactggaa	gggctaattc	1200
actcccaaag	aagacaagat	atccttgatc	tgtggatcta	ccacacacaa	ggctacttcc	1260
ctgattggca	gaactacaca	ccagggccag	gggtcagata	tccactgacc	tttggatggt	1320
gctacaagct	agtaccagtt	gagccagata	aggtagaaga	ggccaataaa	ggagagaaca	1380
ccagcttggt	acaccctgtg	agcctgcatg	ggatggatga	cccggagaga	gaagtgttag	1440
agtggagggt	tgacagccgc	ctagcatttc	atcacgtggc	ccgagagctg	catccggagt	1500
acttcaagaa	ctgctga					1517

<210> 64

<211> 2976

<212> DNA

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 trNef fusion

<400> 64

atggcccagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaaag	gcctacgaca	cgaagtgcga	taacgtgtgg	120
gcgacgcatg	cttgcgtgcc	tacggacccc	aacccccagg	agggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtccct	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaataacg	gctgttttat	aatctcgatg	tgggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tcgcatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	cacccagctg	720
ctgctgaacg	gggtccctggc	tgaggaggag	gtgggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtctgtgg	cgattaaactg	tacccggcct	840
aacaacaaca	cccgtaaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgccca	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cggggggcgag	1080
ttctttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcacccctc	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	ccccccatcg	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320
aacgagacgg	agatcttcag	gcccggcggc	ggcgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaagggtgg	gaagggtggag	ccgctcggcg	tggccccac	ccgggccaag	1440
cgccgcgtcg	tgcagagaat	gggtgcccca	gcttcggtac	tgtctggtgg	agagctggac	1500
agatggggaga	aaattaggct	gcgcccggga	ggcaaaaaga	aatacaagct	caagcatatc	1560
gtgtgggcct	cgaggggagct	tgaacggttt	gccgtgaacc	caggcctgct	ggaaacatct	1620
gagggatgtc	gccagatcct	ggggcaattg	cagccatccc	tccagaccgg	gagtgaagag	1680
ctgaggctcct	tgtataaacac	agtggctacc	ctctactgcg	tacaccagag	gatcagagatt	1740
aaggataacca	aggaggcctt	ggacaaaatt	gaggaggagc	aaaacaagag	caagaagaag	1800
gcccagcagg	cagctgctga	cactgggcat	agcaaccagg	tatcacagaa	ctatcctatt	1860
gtccaaaaca	ttcaggggcca	gatggttcat	caggccatca	gcccccgac	gctcaatgcc	1920
tgggtgaagg	ttgtcgaaga	gaaggccttt	tctcctgagg	ttatcccat	gttctccgct	1980
ttgagtgagg	ggggcactcc	tcaggacctc	aatacaatgc	ttaataaccgt	gggcggccat	2040
caggccgcca	tgcaaatgtt	gaaggagact	atcaacgagg	aggcagccga	gtgggacaga	2100
gtgcatcccg	tccacgctgg	cccaatcgcg	cccggacaga	tgcgggagcc	tcgcggctct	2160

seqlist.txt

```

gacattgccg gcaccacctc tacactgcaa gagcaaatcg gatggatgac caacaatcct 2220
cccatcccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattggt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gcccggctgc caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggacccggac acaaagccag agtggtgatg gtgggttttc cagtcacacc tcaggtacct 2580
ttaagaccaa tgacttataa ggcagctgta gatcttagcc acttttttaa agaaaagggg 2640
ggactggaag ggctaattca ctcccaacga agacaagata tccttgatct gtggatctac 2700
cacacacaag gctacttccc tgattggcag aactacacac cagggccagg ggtagatat 2760
ccactgacct ttggatggtg ctacaagcta gtaccagttg agccagataa ggtagaagag 2820
gccaataaag gagagaacac cagcttgtta caccctgtga gcctgcatgg aatggatgac 2880
cctgagagag aagtgttaga gtggaggttt gacagccgcc tagcatttca tcacgtggcc 2940
cgagagctgc atccggagta cttcaagaac tgctaa 2976

```

<210> 65

<211> 991

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 trNef fusion

<400> 65

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350

```

## seq1ist.txt

His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
				405					410					415	
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly
			420					425					430		
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465					470					475					480
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
				485					490					495	
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
			500					505					510		
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
		515					520					525			
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
	530					535					540				
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
545					550					555					560
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
				565					570					575	
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
			580					585					590		
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
		595					600								
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
	610					615					620				
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
625					630					635					640
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro
				645					650					655	
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
			660					665					670		
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
		675					680					685			
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
	690					695					700				
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
705					710					715					720
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
				725					730					735	
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
			740					745					750		
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
		755					760					765			
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
	770					775					780				
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys
785					790					795					800
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys
				805					810					815	
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met
			820					825					830		
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val
		835					840					845			
Leu	Met	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met
	850					855					860				
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly
865					870					875					880
Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp
				885					890					895	

seqlist.txt

Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr
			900					905					910		
Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr
		915					920					925			
Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly
	930					935					940				
Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp
945					950					955					960
Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe
				965					970					975	
His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	
			980					985					990		

<210> 66  
 <211> 3237  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 trNef Tatm fusion

<400> 66

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaa	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatg	cttgcggtgc	tacggacccc	aacccccagg	aggtgggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtccct	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgatg	tggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tcgcgatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	cacccagctg	720
ctgctgaacg	ggtccctggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtctgtgg	cgattaactg	tacccggcct	840
aacaacaaca	cccgttaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgcca	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggagag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcacccct	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	ccccccatcg	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320
aacgagacgg	agatcttcag	gcccggcggc	ggcgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaaggtggt	gaaggtggag	ccgctcggcg	tggcccccac	ccgggccaag	1440
cgccgcgtcg	tgcagagaa	gggtgcccga	gcttcggtag	tgtctggtgg	agagctggac	1500
agatggggaga	aaattaggct	gcgcccggga	ggcaaaaaga	aatacaagct	caagcatatc	1560
gtgtgggcct	cgagggagct	tgaacggttt	gccgtgaacc	caggcctgct	ggaaacatct	1620
gagggatgtc	gccagatcct	ggggcaattg	cagccatccc	tccagaccgg	gagtgaagag	1680
ctgaggtcct	tgtataacac	agtggctacc	ctctactgcg	tacaccagag	gatcgagatt	1740
aaggatacca	aggaggcctt	ggacaaaatt	gaggaggagc	aaaacaagag	caagaagaag	1800
gcccagcagg	cagctgctga	cactgggcat	agcaaccagg	tatcacagaa	ctatcctatt	1860
gtccaaaaca	ttcaggggcca	gatggttcat	caggccatca	gccccgggac	gctcaatgcc	1920
tgggtgaagg	ttgtcgaaga	gaaggccttt	tctcctgagg	ttatccccat	gttctccgct	1980
ttgagtgagg	gggccacttc	tcaggacctc	aatacaatgc	ttaataaccgt	gggcggccat	2040
caggccgcca	tgcaaatggt	gaaggagact	atcaacgagg	aggcagccga	gtgggacaga	2100
gtgcatcccg	tccacgctgg	cccaatcgcg	cccggacaga	tgcgggagcc	tcgcggctct	2160
gacattgccc	gcaccacctc	tacactgcaa	gagcaaactc	gatggatgac	caacaatcct	2220
cccatcccag	ttggagaaat	ctataaacgg	tggatcattc	tcggtctcaa	taaaattggt	2280
agaatgtact	ctccgacatc	catccttgac	attagacagg	gacccaaaga	gccttttagg	2340
gattacgtcg	accggtttta	taagaccctg	cgagcagagc	aggcctctca	ggaggtcaaa	2400
aactggatga	cggagacact	cctggtacag	aacgctaacc	ccgactgcaa	aacaatcttg	2460
aaggcactag	gcccggctgc	caccctggaa	gagatgatga	ccgcctgtca	gggagtaggc	2520
ggacccggac	acaaagccag	agtgttgatg	gtgggttttc	cagtcacacc	tcaggtagct	2580
ttaagaccaa	tgacttacaa	ggcagctgta	gatcttagcc	acttttttaa	agaaaagggg	2640
ggactggaag	ggctaattca	ctcccaacga	agacaagata	tccttgatct	gtggatctac	2700



## seqlist.txt

```

cacacacaag gctacttccc tgattggcag aactacacac cagggccagg ggtcagatat 2760
ccactgacct ttggatggtg ctacaagcta gtaccagttg agccagataa ggtagaagag 2820
gccaataaag gagagaacac cagcttggtta caccctgtga gcctgcatgg aatggatgac 2880
cctgagagag aagtgttaga gtggagggtt gacagccgcc tagcatttca tcacgtggcc 2940
cgagagctgc atccggagta cttcaagaac tgcactagtg agccagtaga tcctagacta 3000
gagccctgga agcatccagg aagtcagcct aaaactgctt gtaccaattg ctattgtaaa 3060
aagtgttgct ttcattgcca agtttggttc ataacagctg ccttaggcat ctcctatggc 3120
aggaagaagc ggagacagcg acgaagacct cctcaaggca gtcagactca tcaagtttct 3180
ctatcaaagc aaccacacct ccaatccaaa ggggagccga caggcccga ggaataa 3237

```

&lt;210&gt; 67

&lt;211&gt; 1078

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 ds-gp120c p17/24 trNef Tatm fusion

&lt;400&gt; 67

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
      20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
      35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
      50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
      65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
      85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
      100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
      115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
      130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
      145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
      165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
      180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
      195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
      210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
      225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
      245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
      260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
      275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
      290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
      305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
      325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
      340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
      355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
      370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met

```

## seqlist.txt

385	Trp	Gln	Glu	Val	Gly	390	Lys	Ala	Met	Tyr	Ala	395	Pro	Pro	Ile	Gly	Gly	400	Gln
					405						410						415		
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly				
			420					425							430				
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro				
		435						440							445				
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr				
		450						455							460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys				
					470										480				
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly				
				485											495				
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys				
			500					505							510				
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu				
		515						520							525				
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg				
		530				535									540				
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu				
					550										560				
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln				
				565											575				
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu				
			580					585							590				
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr				
		595						600											
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile				
		610						615											
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala				
					630										640				
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro				
				645											655				
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr				
			660					665							670				
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys				
		675						680							685				
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val				
		690				695													
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser				
					710										720				
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met				
				725											735				
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile				
			740					745							750				
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile				
		755						760							765				
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp				
		770						775											
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys				
					790										800				
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys				
				805											815				
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met				
			820					825							830				
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val				
		835						840							845				
Leu	Met	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met				
		850						855							860				
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly				
					870										880				
Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp				
				885											895				
Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr				
			900					905							910				
Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr				
		915						920											
Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly				

## seqlist.txt

930 935 940  
 Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp  
 945 950 955 960  
 Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe  
 965 970 975  
 His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr  
 980 985 990  
 Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
 995 1000 1005  
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
 1010 1015 1020  
 His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly  
 1025 1030 1035 1040  
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
 1045 1050 1055  
 His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu  
 1060 1065 1070  
 Pro Thr Gly Pro Lys Glu  
 1075

<210> 68  
 <211> 3429  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 Nef Tatm fusion

<400> 68  
 atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60  
 accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgca taacgtgtgg 120  
 gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180  
 accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240  
 tctctgtggg accagtccct gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300  
 gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360  
 gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420  
 aaggtgcaga aggaatacgc gctgttttat aatctcgatg tggccccat cgacgacgac 480  
 aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540  
 gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600  
 cctgccggat tcgcatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660  
 accaacgtca gcacggtgca gtgcacccat ggcacccgcc ccgtcgtgag caccagctg 720  
 ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780  
 aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840  
 aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900  
 aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcccc gtggaataac 960  
 accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020  
 aatcagagtt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cgggggagc 1080  
 ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggaac 1140  
 aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200  
 tggcaggagg tgggaaaggc catgtatgcc ccccccacg ggggccaag cggcacggag 1260  
 tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcagcgag 1320  
 aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380  
 ctgtacaagt acaagggtgg gaagggtggag ccgctcggcg tggccccac ccgggccaag 1440  
 cgccgcgtcg tgcagagaat gggtgcccga gcttcggtac tgtctgggtg agagctggac 1500  
 agatgggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560  
 gtgtgggcct cgaggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620  
 gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680  
 ctgaggtcct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740  
 aaggatacca aggaggcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800  
 gccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860  
 gtccaaaaca ttcagggcca gatggttcat caggccatca gccccggac gctcaatgcc 1920  
 tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatccccat gttctccgct 1980  
 ttgagtgaagg gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcggccat 2040  
 caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100  
 gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtct 2160  
 gacattgccg gcaccacctc tacactgcaa gagcaaactc gatggatgac caacaatcct 2220  
 cccatcccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattgtt 2280

seqlist.txt

```

agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gcccggtgc caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggacccggac acaaagccag agtggtgatg ggtggcaagt ggtcaaaaag tagtgtggtt 2580
ggatggccta ctgtaaggga aagaatgaga cgagctgagc cagcagcaga tgggggtggga 2640
gcagcatctc gagacctgga aaaacatgga gcaatcacaa gtagcaatac agcagctacc 2700
aatgctgctt gtgcctggct agaagcacaa gaggaggagg aggtggggtt tccagtcaca 2760
cctcaggtac ctttaagacc aatgacttac aaggcagctg tagatcttag ccacttttta 2820
aaagaaaagg ggggactgga agggctaatt cactcccaac gaagacaaga tatecttgat 2880
ctgtggatct accacacaca aggctacttc cctgattggc agaactacac accagggcca 2940
ggggtcagat atccactgac ctttggatgg tgctacaagc tagtaccagt tgagccagat 3000
aaggtagaag aggccaataa aggagagaac accagcttgt tacaccctgt gagcctgcat 3060
ggaatggatg accctgagag agaagtgtta gagtggagggt ttgacagccg cctagcattt 3120
catcacgtgg cccgagagct gcatccggag tacttcaaga actgcactag tgagccagta 3180
gatcctagac tagagccctg gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat 3240
tgctattgta aaaagtgttg ctttcattgc caagtttgtt tcataacagc tgccttaggc 3300
atctcctatg gcaggaagaa gcggagacag cgacgaagac ctctcaagg cagtcagact 3360
catcaagttt ctctatcaaa gcaaccacc tcccaatcca aaggggagcc gacaggccc 3420
aaggaataa

```

<210> 69

<211> 1142

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 Nef Tatm fusion

<400> 69

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1          5          10          15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20          25          30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35          40          45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50          55          60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65          70          75          80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85          90          95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100          105          110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115          120          125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130          135          140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145          150          155          160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165          170          175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180          185          190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195          200          205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210          215          220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225          230          235          240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245          250          255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260          265          270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275          280          285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290          295          300

```



## seqlist.txt

Asp 305	Ile	Arg	Gln	Ala	His 310	Cys	Asn	Leu	Ser	Arg 315	Ala	Gln	Trp	Asn	Asn 320
Thr	Leu	Lys	Gln	Ile 325	Val	Ile	Lys	Leu	Arg 330	Glu	His	Phe	Gly	Asn 335	Lys
Thr	Ile	Lys	Phe 340	Asn	Gln	Ser	Ser	Gly 345	Gly	Asp	Pro	Glu	Ile 350	Val	Arg
His	Ser	Phe 355	Asn	Cys	Gly	Gly	Glu 360	Phe	Phe	Tyr	Cys	Asp 365	Thr	Thr	Gln
Leu	Phe 370	Asn	Ser	Thr	Trp	Asn 375	Gly	Thr	Glu	Gly	Asn 380	Asn	Thr	Glu	Gly
Asn 385	Ser	Thr	Ile	Thr	Leu 390	Pro	Cys	Arg	Ile	Lys 395	Gln	Ile	Ile	Asn	Met 400
Trp	Gln	Glu	Val	Gly 405	Lys	Ala	Met	Tyr	Ala 410	Pro	Pro	Ile	Gly	Gly 415	Gln
Ile	Arg	Cys	Ser 420	Ser	Asn	Ile	Thr	Gly 425	Leu	Leu	Leu	Thr	Arg 430	Asp	Gly
Gly	Thr	Glu 435	Gly	Asn	Gly	Thr	Glu 440	Asn	Glu	Thr	Glu	Ile 445	Phe	Arg	Pro
Gly	Gly 450	Gly	Asp	Met	Arg	Asp 455	Asn	Trp	Arg	Ser	Glu 460	Leu	Tyr	Lys	Tyr
Lys 465	Val	Val	Lys	Val	Glu 470	Pro	Leu	Gly	Val	Ala 475	Pro	Thr	Arg	Ala	Lys 480
Arg	Arg	Val	Val	Gln 485	Arg	Met	Gly	Ala	Arg 490	Ala	Ser	Val	Leu	Ser 495	Gly
Gly	Glu	Leu	Asp 500	Arg	Trp	Glu	Lys	Ile 505	Arg	Leu	Arg	Pro	Gly 510	Gly	Lys
Lys	Lys	Tyr 515	Lys	Leu	Lys	His	Ile 520	Val	Trp	Ala	Ser	Arg 525	Glu	Leu	Glu
Arg	Phe 530	Ala	Val	Asn	Pro	Gly 535	Leu	Leu	Glu	Thr	Ser 540	Glu	Gly	Cys	Arg
Gln 545	Ile	Leu	Gly	Gln	Leu 550	Gln	Pro	Ser	Leu	Gln 555	Thr	Gly	Ser	Glu	Glu 560
Leu	Arg	Ser	Leu	Tyr 565	Asn	Thr	Val	Ala	Thr 570	Leu	Tyr	Cys	Val	His 575	Gln
Arg	Ile	Glu	Ile 580	Lys	Asp	Thr	Lys	Glu 585	Ala	Leu	Asp	Lys	Ile 590	Glu	Glu
Glu	Gln	Asn 595	Lys	Ser	Lys	Lys	Lys 600	Ala	Gln	Gln	Ala	Ala 605	Ala	Asp	Thr
Gly	His 610	Ser	Asn	Gln	Val	Ser 615	Gln	Asn	Tyr	Pro	Ile 620	Val	Gln	Asn	Ile
Gln 625	Gly	Gln	Met	Val	His 630	Gln	Ala	Ile	Ser	Pro 635	Arg	Thr	Leu	Asn	Ala 640
Trp	Val	Lys	Val	Val 645	Glu	Glu	Lys	Ala	Phe 650	Ser	Pro	Glu	Val	Ile 655	Pro
Met	Phe	Ser	Ala 660	Leu	Ser	Glu	Gly	Ala 665	Thr	Pro	Gln	Asp	Leu 670	Asn	Thr
Met	Leu	Asn 675	Thr	Val	Gly	Gly	His 680	Gln	Ala	Ala	Met	Gln 685	Met	Leu	Lys
Glu	Thr 690	Ile	Asn	Glu	Glu	Ala 695	Ala	Glu	Trp	Asp	Arg 700	Val	His	Pro	Val
His 705	Ala	Gly	Pro	Ile	Ala 710	Pro	Gly	Gln	Met	Arg 715	Glu	Pro	Arg	Gly	Ser 720
Asp	Ile	Ala	Gly	Thr 725	Thr	Ser	Thr	Leu	Gln 730	Glu	Gln	Ile	Gly	Trp 735	Met
Thr	Asn	Asn	Pro 740	Pro	Ile	Pro	Val	Gly 745	Glu	Ile	Tyr	Lys	Arg 750	Trp	Ile
Ile	Leu	Gly 755	Leu	Asn	Lys	Ile	Val 760	Arg	Met	Tyr	Ser	Pro 765	Thr	Ser	Ile
Leu	Asp 770	Ile	Arg	Gln	Gly	Pro 775	Lys	Glu	Pro	Phe	Arg 780	Asp	Tyr	Val	Asp
Arg 785	Phe	Tyr	Lys	Thr	Leu 790	Arg	Ala	Glu	Gln	Ala 795	Ser	Gln	Glu	Val	Lys 800
Asn	Trp	Met	Thr	Glu 805	Thr	Leu	Leu	Val	Gln 810	Asn	Ala	Asn	Pro	Asp 815	Cys
Lys	Thr	Ile	Leu 820	Lys	Ala	Leu	Gly	Pro 825	Ala	Ala	Thr	Leu	Glu 830	Glu	Met
Met	Thr	Ala 835	Cys	Gln	Gly	Val	Gly 840	Gly	Pro	Gly	His	Lys 845	Ala	Arg	Val

## seqlist.txt

Leu Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr  
 850 855 860  
 Val Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly  
 865 870 875 880  
 Ala Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn  
 885 890 895  
 Thr Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu  
 900 905 910  
 Glu Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met  
 915 920 925  
 Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly  
 930 935 940  
 Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp  
 945 950 955 960  
 Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr  
 965 970 975  
 Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr  
 980 985 990  
 Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly  
 995 1000 1005  
 Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp  
 1010 1015 1020  
 Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe  
 1025 1030 1035 1040  
 His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr  
 1045 1050 1055  
 Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
 1060 1065 1070  
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
 1075 1080 1085  
 His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly  
 1090 1095 1100  
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
 1105 1110 1115 1120  
 His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu  
 1125 1130 1135  
 Pro Thr Gly Pro Lys Glu  
 1140

<210> 70  
 <211> 3426  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 mNef Tatm fusion

<400> 70  
 atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60  
 accaccctct tctgcgcgag cgacgccaaag gcctacgaca cggaagtgca taacgtgtgg 120  
 gcgacgcattg cttgcgtgcc tacggacccc aacccccagg aggtgggtgct gggaaacgtg 180  
 accgagtact tcaacatgtg gaagaataac atgggtggatc agatgcacga ggacatcatc 240  
 tctctgtggg accagtccct gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300  
 gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360  
 gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420  
 aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtcccat cgacgacgac 480  
 aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540  
 gtcattgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600  
 cctgccggat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660  
 accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720  
 ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780  
 aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840  
 aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgccgcg 900  
 aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgccca gtggaataac 960  
 accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020  
 aatcagagtt ctggcgagga ccccgagatc gtgcggcact ccttcaactg cgggggagag 1080  
 ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggaac 1140

seqlist.txt

```

aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacgc ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaaggtggt gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgctc tgcagagaat gggtgcccga gcttcggtac tgtctggtgg agagctggac 1500
agatgggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560
gtgtgggcct cgagggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620
gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggtcct tgtataacac agtggctacc ctctactgcy tacaccagag gatcgagatt 1740
aaggatacca aggaggcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800
gcccgacgag cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860
gtccaaaaca ttcagggcca gatggttcac caggccatca gcccccgac gctcaatgcc 1920
tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatcccat gttctccgct 1980
ttgagtgagg gggccactcc tcaggacctc aatacaatgc ttaataaccgt gggcggccat 2040
caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100
gtgcatcccg tccacgctgg cccaatcgcy cccggacaga tgcgggagcc tcgcggtctt 2160
gacattgccg gcaccacctc tacactgcaa gagcaaatcy gatggatgac caacaatcct 2220
cccatcccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattggt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gcccggtgct caccctggaa gagatgatga ccgctgtca gggagtaggc 2520
ggacccggac acaaagccag agtggtgatg ggcaagtggc caaaaagtag tgtggttga 2580
tggcctactg taagggaaag aatgagacga gctgagccag cagcagatgg ggtgggagca 2640
gcatctcgag acctggaaaa acatggagca atcacaaagta gcaatacagc agctaccaat 2700
gctgcttggt cctggctaga agcacaagag gaggaggagg tgggttttcc agtcacacct 2760
caggtacctt taagaccaat gacttacaag gcagctgtag atcttagcca ctttttaaaa 2820
gaaaaggggg gactggaagg gctaattcac tcccaacgaa gacaagatat ccttgatctg 2880
tggatctacc acacacaagg ctacttcctt gattggcaga actacacacc agggccaggg 2940
gtcagatatc cactgacctt tggatggtgc tacaagctag taccagttga gccagataag 3000
gtagaagagg ccaataaagg agagaacacc agcttggtac accctgtgag cctgcatgga 3060
atggatgacc ctgagagaga agtggttagag tggaggtttg acagccgcct agcatttcat 3120
cacgtggccc gagagctgca tccggagtag ttcaagaact gcactagtga gccagtagat 3180
cctagactag agccctggaa gcatccagga agtcagccta aaactgcttg taccaattgc 3240
tattgtaaaa agtggtgctt tcattgccaa gtttgtttca taacagctgc cttaggcatc 3300
tcctatggca ggaagaagcg gagacagcga cgaagacctc ctcaaggcag tcagactcat 3360
caagtttctc tatcaaagca acccacctcc caatccaaag gggagccgac aggcccgaag 3420
gaataa

```

<210> 71

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mNef Tatm fusion

<400> 71

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1           5           10          15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
           20           25           30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
           35           40           45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
           50           55           60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65           70           75           80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
           85           90           95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
           100          105          110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
           115          120          125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
           130          135          140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp

```

## seqlist.txt

145	Asn	Ala	Thr	Thr	Lys	150	Asn	Lys	Thr	Thr	Arg	155	Asn	Phe	Arg	Leu	Ile	160	His
					165						170						175		
	Cys	Asn	Ser	Ser	Val	Met	Thr	Gln	Ala	185	Cys	Pro	Lys	Val	Ser	190	Phe	Glu	
	Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	200	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys		
			195											205					
	Cys	Asn	Asn	Lys	Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser			
		210					215						220						
	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu			
225						230						235							
	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp			
					245														
	Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser			
				260															
	Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile			
			275																
	His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly			
		290					295												
	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn			
305						310													
	Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys			
					325														
	Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg			
				340															
	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln			
			355																
	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly			
							375												
	Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met			
385						390													
	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln			
					405														
	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly			
				420															
	Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro			
				435															
	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr			
		450					455												
	Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys			
465						470													
	Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly			
					485														
	Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys			
				500															
	Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu			
	Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg			
							535												
	Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu			
545						550													
	Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln			
					565														
	Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu			
				580															
	Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr			
				595															
	Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile			
		610					615												
	Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala			
625						630													
	Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro			
					645														
	Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr			
				660															
	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys			
				675															
	Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val			



## seqlist.txt

```

690      695      700
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705      710      715      720
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725      730      735
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740      745      750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755      760      765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770      775      780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785      790      795      800
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805      810      815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820      825      830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835      840      845
Leu Met Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val
850      855      860
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
865      870      875      880
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
885      890      895
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
900      905      910
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
915      920      925
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
930      935      940
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
945      950      955      960
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
965      970      975
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
980      985      990
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
995      1000      1005
Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
1010      1015      1020
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
1025      1030      1035      1040
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
1045      1050      1055
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
1060      1065      1070
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
1075      1080      1085
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
1090      1095      1100
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
1105      1110      1115      1120
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
1125      1130      1135
Thr Gly Pro Lys Glu
1140

```

&lt;210&gt; 72

&lt;211&gt; 3429

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 ds-gp120c p17/24 L1-Nef Tatm fusion

&lt;400&gt; 72

seqlist.txt

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaa	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatg	cttgcggtgc	tacggacccc	aacccccagg	aggtgggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtccct	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaaac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcga	tgggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgccggat	tcgcgatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacgggtga	gtgcacccat	ggcatccgcc	ccgtcgtgag	cacccagctg	720
ctgctgaacg	ggtccctggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtcgtgtg	cgattaactg	tacccggcct	840
aacaacaaca	cccgtgaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgcca	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggcgag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcaccttc	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	ccccccatcg	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320
aacgagacgg	agatcttcag	gcccggcggc	ggcgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaaggtggg	gaaggtggag	ccgctcggcg	tggcccccac	ccgggccaag	1440
cgccgcgtcg	tgagagaaat	gggtgcccga	gcttcgggtac	tgtctgggtg	agagctggac	1500
agatgggaga	aaattaggct	gcgcccggga	ggcaaaaaga	aatacaagct	caagcatatc	1560
gtgtgggcct	cgaggggagct	tgaacggttt	gccgtgaacc	caggcctgct	ggaaacatct	1620
gagggatgtc	gccagatcct	ggggcaattg	cagccatccc	tccagaccgg	gagtgaagag	1680
ctgaggtcct	tgtataaac	agtggctacc	ctctactgcg	tacaccagag	gatcgagatt	1740
aaggatacca	aggaggcctt	ggacaaaatt	gaggaggagc	aaaacaagag	caagaagaag	1800
gcccagcagg	cagctgctga	cactgggcat	agcaaccagg	tatcacagaa	ctatcctatt	1860
gtccaaaaca	ttcaggggcca	gatggttcat	caggccatca	gccccgggac	gctcaatgcc	1920
tgggtgaagg	ttgtcgaaga	gaaggccttt	tctcctgagg	ttatccccat	gttctccgct	1980
ttgagtgaagg	gggcccactcc	tcaggacctc	aatacaatgc	ttaataccgt	gggcggccat	2040
caggccgcca	tgcaaagtgt	gaaggagact	atcaacgagg	aggcagccga	gtgggacaga	2100
gtgcatcccg	tccacgctgg	cccaatcgcg	cccggacaga	tgcgggagcc	tcgcggctct	2160
gacattgccg	gcaccacctc	tacactgcaa	gagcaaatcg	gatggatgac	caacaatcct	2220
cccattcccag	ttggagaaat	ctataaacgg	tggatcattc	tcggtctcaa	taaaattggt	2280
agaatgtact	ctccgacatc	catccttgac	attagacagg	gacccaaaga	gccttttagg	2340
gattacgtcg	accggtttta	taagaccctg	cgagcagagc	aggcctctca	ggaggtcaaa	2400
aactggatga	cggagacact	cctggtacag	aacgctaacc	ccgactgcaa	aacaatcttg	2460
aaggcactag	gcccggctgc	caccctggaa	gagatgatga	ccgcctgtca	gggagtaggc	2520
ggacccggac	acaaagccag	agtgtttgat	ggtggcaagt	ggtcaaaaag	tagtgtggtt	2580
ggatggccta	ctgtaaggga	aagaatgaga	cgagctgagc	cagcagcaga	tgggggtggga	2640
gcagcatctc	gagacctgga	aaaacatgga	gcaatcacia	gtagcaatac	agcagctacc	2700
aatgctgctt	gtgcctggct	agaagcacia	gaggaggagg	aggtgggttt	tccagtcaca	2760
cctcaggtac	ctttaagacc	aatgacttac	aaggcagctg	tagatcttag	ccacttttta	2820
aaagaaaagg	ggggactgga	agggttaatt	cactcccaac	gaagacaaga	tatccttgat	2880
ctgtggatct	accacacaca	aggctacttc	cctgattggc	agaactacac	accagggcca	2940
ggggtcagat	atccactgac	ctttggatgg	tgctacaagc	tagtaccagt	tgagccagat	3000
aaggtagaag	aggccaataa	aggagagaac	accagcgcct	tacaccctgt	gagcctgcat	3060
ggaatggatg	accctgagag	agaagtgtta	gagtggagg	ttgacagccg	cctagcattt	3120
catcacgtgg	cccagagagc	gcatccggag	tacttcaaga	actgcactag	tgagccagta	3180
gacccatagc	tagagccctg	gaagcatcca	ggaagtcagc	ctaaaactgc	ttgtaccaat	3240
tgctattgta	aaaagtgttg	ctttcattgc	caagtttgtt	tcataacagc	tgcccttaggc	3300
atctcctatg	gcaggaagaa	gcggagacag	cgacgaagac	ctcctcaagg	cagtcagact	3360
catcaagttt	ctctatcaaa	gcaacccacc	tccaatcca	aaggggagcc	gacaggcccg	3420
aaggaataa						3429

<210> 73

<211> 1142

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 L1-Nef Tatm fusion

<400> 73

seq1ist.txt

Met	Ala	Glu	Gln	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp
1				5					10					15	
Lys	Glu	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr
			20					25					30		
Asp	Thr	Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr
		35					40					45			
Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Tyr	Phe
	50					55					60				
Asn	Met	Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile
65				70					75					80	
Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu
			85						90					95	
Cys	Val	Thr	Leu	Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Asn	Ser	Thr	Thr
			100					105					110		
Thr	Thr	Ser	Asn	Gly	Trp	Thr	Gly	Glu	Ile	Arg	Lys	Gly	Glu	Ile	Lys
		115					120					125			
Asn	Cys	Ser	Phe	Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys
	130					135					140				
Glu	Tyr	Ala	Leu	Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp
145					150					155					160
Asn	Ala	Thr	Thr	Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His
				165					170					175	
Cys	Asn	Ser	Ser	Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu
			180					185					190		
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys
		195					200					205			
Cys	Asn	Asn	Lys	Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser
	210					215					220				
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu
225					230					235					240
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp
			245					250						255	
Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser
			260					265					270		
Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile
		275					280					285			
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
	290					295					300				
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
305					310					315					320
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
			325						330				335		
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
				405					410					415	
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly
			420					425					430		
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465					470					475					480
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
				485					490					495	
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
			500					505					510		
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
		515					520					525			
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
	530					535					540				

## seqlist.txt

Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
545					550					555					560
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
				565					570					575	
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
			580					585					590		
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
		595					600				605				
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
	610					615					620				
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
625					630					635					640
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro
				645					650					655	
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
			660					665					670		
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
		675					680					685			
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
	690					695					700				
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
705					710					715					720
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
				725					730					735	
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
			740					745					750		
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
		755					760					765			
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
	770					775					780				
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys
785					790					795					800
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys
				805					810					815	
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met
			820					825					830		
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val
		835					840					845			
Leu	Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr
	850					855					860				
Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly
865					870					875					880
Ala	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn
				885					890					895	
Thr	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu
			900					905					910		
Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met
		915					920					925			
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly
	930					935					940				
Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp
945					950					955					960
Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr
				965					970					975	
Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr
			980					985					990		
Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly
		995					1000					1005			
Glu	Asn	Thr	Ser	Ala	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp
	1010					1015					1020				
Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe
1025					1030					1035					1040
His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr
				1045					1050					1055	
Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser
			1060					1065					1070		
Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe
		1075					1080					1085			



seqlist.txt

His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly  
 1090 1095 1100  
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
 1105 1110 1115 1120  
 His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu  
 1125 1130 1135  
 Pro Thr Gly Pro Lys Glu  
 1140

<210> 74  
 <211> 3429  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 L2-Nef Tatm fusion

<400> 74  
 atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60  
 accaccctct tctgcgcgag cgacgccaaag gcctacgaca cggaagtgca taacgtgtgg 120  
 gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180  
 accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240  
 tctctgtggg accagtccct gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300  
 gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360  
 gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420  
 aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtcccat cgacgacgac 480  
 aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540  
 gtcattgacg aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600  
 cctgccggat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660  
 accaactgca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720  
 ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780  
 aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840  
 aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgccgc 900  
 aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960  
 accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020  
 aatcagagtt ctggcgagga ccccgagatc gtgcggcact ccttcaactg cgggggagc 1080  
 ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggaac 1140  
 aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200  
 tggcaggagg tgggaaaggc catgtatgcc ccccccattc ggggacagat ccgctgctcc 1260  
 tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320  
 aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380  
 ctgtacaagt acaagggtgt gaagggtggag ccgctcggcg tggccccac ccgggccaag 1440  
 cgccgcgtcg tgcagagaat ggggtgcccg gcttcggtac tgtctggtgg agagctggac 1500  
 agatgggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560  
 gtgtgggcct cgaggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620  
 gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680  
 ctgaggtcct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740  
 aaggatacca aggaggcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800  
 gccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860  
 gtccaaaaca ttcagggcca gatggttcat caggccatca gccccggac gctcaatgcc 1920  
 tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatcccat gttctccgct 1980  
 ttgagtgaagg gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcgccat 2040  
 caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100  
 gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtct 2160  
 gacattgccg gcaccacctc tacactgcaa gagcaaatcg gatggatgac caacaatcct 2220  
 cccatcccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattgtt 2280  
 agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340  
 gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggagggtcaa 2400  
 aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460  
 aaggcactag gcccggtgc caccctggaa gagatgatga ccgcctgtca gggagttagg 2520  
 ggacccggac acaaagccag agtggtgatg ggtggcaagt ggtcaaaaag tagtgtggtt 2580  
 ggatggccta ctgtaaggga aagaatgaga cgagctgagc cagcagcaga tgggggtggga 2640  
 gcagcatctc gagacctgga aaaacatgga gcaatcaca gtagcaatac agcagctacc 2700  
 aatgctgctt gtgcctggct agaagcaca gaggaggagg aggtgggttt tccagtcaca 2760  
 cctcaggtac ctttaagacc aatgacttac aaggcagctg tagatcttag ccacttttta 2820  
 aaagaaaagg ggggactgga agggctaatt cactcccaac gaagacaaga tatccttgat 2880  
 ctgtggatct accacacaca aggctacttc cctgattggc agaactacac accagggcca 2940

seqlist.txt

```

ggggtcagat atccactgac ctttggatgg tgctacaagc tagtaccagt tgagccagat 3000
aaggtagaag aggccaataa aggagagaac accagcttgg cacaccctgt gagcctgcat 3060
ggaatggatg accctgagag agaagtgtta gagtggaggt ttgacagccg cctagcattt 3120
catcacgtgg cccgagagct gcatccggag tacttcaaga actgcactag tgagccagta 3180
gacccctagac tagagccctg gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat 3240
tgctattgta aaaagtgttg ctttcattgc caagtttgtt tcataacagc tgccttaggc 3300
atctcctatg gcaggaagaa gcggagacag cgacgaagac ctcctcaagg cagtcagact 3360
catcaagttt ctctatcaaa gcaaccacc tcccaatcca aaggggagcc gacaggcccg 3420
aaggaataa 3429

```

<210> 75  
 <211> 1142  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 L2-Nef Tatm fusion

<400> 75

Met	Ala	Glu	Gln	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp
1				5					10					15	
Lys	Glu	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr
			20					25					30		
Asp	Thr	Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr
		35				40						45			
Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Tyr	Phe
	50				55					60					
Asn	Met	Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile
65				70					75					80	
Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu
			85					90						95	
Cys	Val	Thr	Leu	Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Asn	Ser	Thr	Thr
			100					105					110		
Thr	Thr	Ser	Asn	Gly	Trp	Thr	Gly	Glu	Ile	Arg	Lys	Gly	Glu	Ile	Lys
		115					120					125			
Asn	Cys	Ser	Phe	Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys
	130					135					140				
Glu	Tyr	Ala	Leu	Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp
145				150					155					160	
Asn	Ala	Thr	Thr	Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His
			165					170						175	
Cys	Asn	Ser	Ser	Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu
			180					185					190		
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys
		195					200					205			
Cys	Asn	Asn	Lys	Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser
	210					215					220				
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu
225				230					235						240
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp
			245					250						255	
Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser
			260					265					270		
Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile
		275					280					285			
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
	290					295					300				
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
305				310					315					320	
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
			325					330						335	
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met

seqlist.txt																			
385											390				395				400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln				
				405					410					415					
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly				
			420					425					430						
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro				
		435					440					445							
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr				
	450					455					460								
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys				
465					470					475					480				
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly				
				485					490					495					
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys				
			500					505					510						
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu				
		515					520					525							
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg				
	530					535					540								
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu				
545					550					555					560				
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln				
				565					570					575					
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu				
			580					585					590						
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr				
		595					600					605							
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile				
	610					615					620								
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala				
625					630					635					640				
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro				
				645					650					655					
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr				
			660					665					670						
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys				
		675					680					685							
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val				
	690					695					700								
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser				
705					710					715					720				
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met				
				725					730					735					
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile				
			740					745					750						
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile				
		755					760					765							
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp				
	770					775					780								
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys				
785					790					795					800				
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys				
				805					810					815					
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met				
			820					825					830						
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val				
		835					840					845							
Leu	Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr				
	850					855					860								
Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly				
865					870					875					880				
Ala	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn				
				885					890					895					
Thr	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu				
			900					905					910						
Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met				
		915					920					925							
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly				

seqlist.txt

```

930          935          940
Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp
945          950          955          960
Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr
          965          970          975
Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr
          980          985          990
Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly
          995          1000          1005
Glu Asn Thr Ser Leu Ala His Pro Val Ser Leu His Gly Met Asp Asp
          1010          1015          1020
Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe
          1025          1030          1035          1040
His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr
          1045          1050          1055
Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
          1060          1065          1070
Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
          1075          1080          1085
His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly
          1090          1095          1100
Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
          1105          1110          1115          1120
His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu
          1125          1130          1135
Pro Thr Gly Pro Lys Glu
          1140

```

<210> 76  
 <211> 3429  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 LL-Nef Tatm fusion

```

<400> 76
atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60
accaccctct tctgcgcgag cgacgccaaag gcctacgaca cggaagtgca taacgtgtgg 120
gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtccct gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtcccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgccgcg 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcccc gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cgggggagcg 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcaccttc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc cccccatcg ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgg gaaggtggag ccgctcggcg tggcccccac ccgggccaa 1440
cgccgcgtcg tgcagagaaat ggggtgcccg gcttcgggtac tgtctgggtg agagctggac 1500
agatggggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560
gtgtgggcct cgagggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620
gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggtcct tgtataaacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740
aaggatacca aggaggcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800

```



seqlist.txt

```

gcccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860
gtccaaaaca ttcagggcca gatgggttcat caggccatca gcccccgac gctcaatgcc 1920
tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatcccat gttctccgct 1980
ttgagtgagg gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcggccat 2040
caggccgcca tgcaaatggt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100
gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtct 2160
gacattgccg gcaccacctc tacactgcaa gagcaaatcg gatggatgac caacaatcct 2220
cccatcccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattggt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gcccggtgc caccctggaa gagatgatga ccgctgtca gggagttagg 2520
ggacccggac acaaagccag agtggtgatg ggtggcaagt ggtcaaaaag tagtgtggt 2580
ggatggccta ctgtaaggga aagaatgaga cgagctgagc cagcagcaga tggggtggga 2640
gcagcatctc gagacctgga aaaacatgga gcaatcacia gtagcaatac agcagctacc 2700
aatgctgctt gtgcctggct agaagcacia gaggaggagg aggtgggttt tccagtcaca 2760
cctcaggtac ctttaagacc aatgacttac aaggcagctg tagatcttag ccacttttta 2820
aaagaaaagg ggggactgga agggctaatt cactcccaac gaagacaaga tatccttgat 2880
ctgtggatct accacacaca aggtacttc cctgattggc agaactacac accagggcca 2940
ggggtcagat atccactgac ctttggatgg tgctacaagc tagtaccagt tgagccagat 3000
aaggtagaag aggccaataa aggagagaac accagcgccg cacaccctgt gagcctgcat 3060
ggaatggatg accctgagag agaagtgtta gagtggagg ttgacagccg cctagcattt 3120
catcacgtgg cccgagagct gcatccggag tacttcaaga actgcactag tgagccagta 3180
gatcctagac tagagccctg gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat 3240
tgctattgta aaaagtgttg ctttcattgc caagtgtgtt tcataacagc tgccttaggc 3300
atctcctatg gcaggaagaa gcggagacag cgacgaagac ctctcaagg cagtcagact 3360
catcaagttt ctctatcaaa gcaaccacc tcccaatcca aaggggagcc gacaggccc 3420
aaggaataa 3429

```

<210> 77

<211> 1142

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 LL-Nef Tatm fusion

<400> 77

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75     80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115    120    125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145    150    155    160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165    170    175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180    185    190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195    200    205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210    215    220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225    230    235    240

```

Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp
				245					250					255	
Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser
			260					265					270		
Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile
		275					280					285			
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
	290					295					300				
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
305					310					315					320
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
			325						330					335	
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
			405						410					415	
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly
			420					425					430		
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465					470					475					480
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
			485						490					495	
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
			500					505					510		
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
		515					520					525			
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
	530					535					540				
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
545					550					555					560
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
			565						570					575	
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
			580					585					590		
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
		595					600					605			
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
	610					615					620				
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
625					630					635					640
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro
			645						650					655	
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
			660					665					670		
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
		675					680					685			
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
	690					695					700				
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
705					710					715					720
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
			725						730					735	
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
			740					745					750		
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
		755					760					765			
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
	770					775					780				

seqlist.txt

Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys
785					790				795						800
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys
			805						810					815	
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met
			820					825					830		
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val
		835					840					845			
Leu	Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr
	850					855					860				
Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly
865					870					875					880
Ala	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn
				885					890					895	
Thr	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu
			900					905					910		
Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met
		915					920					925			
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly
	930					935					940				
Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp
945					950					955					960
Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr
				965					970					975	
Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr
			980					985					990		
Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly
		995					1000					1005			
Glu	Asn	Thr	Ser	Ala	Ala	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp
	1010					1015					1020				
Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe
1025					1030					1035					1040
His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr
				1045					1050					1055	
Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser
			1060					1065					1070		
Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe
		1075					1080					1085			
His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr	Gly
	1090					1095					1100				
Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr
1105					1110					1115					1120
His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Lys	Gly	Glu
				1125					1130					1135	
Pro	Thr	Gly	Pro	Lys	Glu										
			1140												

<210> 78  
 <211> 3426  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 mLL-Nef Tatm fusion

<400> 78  
 atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60  
 accaccctct tctgcgcgag cgacgccaaag gcctacgaca cggaagtgca taacgtgtgg 120  
 gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180  
 accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240  
 tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300  
 gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360  
 gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420  
 aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtcccat cgacgacgac 480  
 aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540  
 gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600  
 cctgccggat tcgcgatacct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660

seqlist.txt

```

accaaactgca gcacgggtgca gtgcacccat ggcatccgcc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cgggggag 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcacctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacg ggggagcagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgt gaagggtggg ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagaaat ggggtgccga gcttcggtac tgtctggtgg agagctggac 1500
agatgggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560
gtgtgggcct cgagggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620
gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggtcct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740
aaggatacca aggaggcctt ggacaaaatt gagggaggagc aaaacaagag caagaagaag 1800
gcccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860
gtccaaaaca ttcagggcca gatggttcat caggccatca gccccggac gctcaatgcc 1920
tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatcccat gttctccgct 1980
ttgagtgaagg gggccactcc tcaggacctc aatacaatgc ttaataaccgt gggcgcccat 2040
caggccgcca tgcaaatggt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100
gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtct 2160
gacattgccg gcaccacctc tacttgcaa gagcaaatcg gatggatgac caacaatcct 2220
cccatcccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattgtt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gcccggtgct caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggacccggac acaaagccag agtggtgatg ggcaagtggc caaaaagtag tgtggttga 2580
tggcctactg taagggaaag aatgagacga gctgagccag cagcagatgg ggtgggagca 2640
gcatctcgag acctggaaaa acatggagca atcacaagta gcaatacagc agctaccaat 2700
gctgcttggt cctggctaga agcacaagag gagggaggag tgggttttcc agtcacacct 2760
caggtacctt taagaccaat gacttacaag gcagctgtag atcttagcca ctttttaaaa 2820
gaaaaggggg gactggaagg gctaattcac tcccaacgaa gacaagatat ccttgatctg 2880
tgatctacc acacacaagg ctacttcctt gattggcaga actacacacc agggccaggg 2940
gtcagatatc cactgacctt tggatggtgc tacaagctag taccagttga gccagataag 3000
gtagaagagg ccaataaagg agagaacacc agcgccgcac accctgtgag cctgcatgga 3060
atggatgacc ctgagagaga agtggttagag tggaggtttg acagccgcct agcatttcat 3120
cacgtggccc gagagctgca tccggagtac ttcaagaact gcactagtga gccagtagat 3180
cctagactag agccctggaa gcattccagga agtcagccta aaactgcttg taccaattgc 3240
tattgtaaaa agtggtgctt tcattgccaa gtttgtttca taacagctgc cttaggcatc 3300
tcctatggca ggaagaagcg gagacagcga cgaagacctc ctcaaggcag tcagactcat 3360
caagtttctc tatcaaagca acccacctcc caatccaaag gggagccgac aggcccgaag 3420
gaataa 3426

```

<210> 79

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mLL-Nef Tatm fusion

<400> 79

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10     15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75     80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu

```



## seqlist.txt

				85					90					95		
Cys	Val	Thr	Leu	Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Asn	Ser	Thr	Thr	
			100					105					110			
Thr	Thr	Ser	Asn	Gly	Trp	Thr	Gly	Glu	Ile	Arg	Lys	Gly	Glu	Ile	Lys	
		115					120					125				
Asn	Cys	Ser	Phe	Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys	
	130					135					140					
Glu	Tyr	Ala	Leu	Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp	
145					150					155					160	
Asn	Ala	Thr	Thr	Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His	
				165					170					175		
Cys	Asn	Ser	Ser	Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu	
			180					185					190			
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys	
		195					200					205				
Cys	Asn	Asn	Lys	Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser	
	210					215					220					
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	
225					230					235					240	
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp	
				245						250				255		
Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	
			260					265					270			
Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	
		275					280					285				
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly	
	290					295					300					
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn	
305					310					315					320	
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys	
				325						330				335		
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg	
			340					345					350			
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln	
		355					360					365				
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly	
	370					375					380					
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met	
385					390					395					400	
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	
				405					410					415		
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	
			420					425					430			
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro	
		435					440					445				
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	
	450					455					460					
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	
465					470					475					480	
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	
				485					490					495		
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	
			500					505					510			
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	
		515					520					525				
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	
	530					535					540					
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	
545					550					555					560	
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	
				565					570					575		
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	
			580					585					590			
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	
		595					600					605				
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	
	610					615					620					
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	

```

                                seqlist.txt
625                               630                               635                               640
Trp val Lys val val Glu Glu Lys Ala Phe Ser Pro Glu val Ile Pro
645                               650
Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660                               665
Met Leu Asn Thr val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675                               680
Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val
690                               695
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705                               710
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725                               730
Thr Asn Asn Pro Pro Ile Pro val Gly Glu Ile Tyr Lys Arg Trp Ile
740                               745
Ile Leu Gly Leu Asn Lys Ile val Arg Met Tyr Ser Pro Thr Ser Ile
755                               760
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770                               775
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785                               790
Asn Trp Met Thr Glu Thr Leu Leu val Gln Asn Ala Asn Pro Asp Cys
805                               810
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820                               825
Met Thr Ala Cys Gln Gly val Gly Gly Pro Gly His Lys Ala Arg val
835                               840
Leu Met Gly Lys Trp Ser Lys Ser Ser val val Gly Trp Pro Thr val
850                               855
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly val Gly Ala
865                               870
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
885                               890
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
900                               905
Glu val Gly Phe Pro val Thr Pro Gln val Pro Leu Arg Pro Met Thr
915                               920
Tyr Lys Ala Ala val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
930                               935
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
945                               950
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
965                               970
Pro Gly Pro Gly val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
980                               985
Leu val Pro val Glu Pro Asp Lys val Glu Glu Ala Asn Lys Gly Glu
995                               1000
Asn Thr Ser Ala Ala His Pro val Ser Leu His Gly Met Asp Asp Pro
1010                               1015
Glu Arg Glu val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
1025                               1030
His val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
1045                               1050
Glu Pro val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
1060                               1065
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Phe His
1075                               1080
Cys Gln val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
1090                               1095
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
1105                               1110
Gln val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
1125                               1130
Thr Gly Pro Lys Glu
1140                               1135

```



seqlist.txt

<211> 3426  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> HIV-1 ds-gp120c p17/24 mL1-Nef Tatm fusion

<400> 80

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaag	gcctacgaca	cggaagtgca	taacgtgtgg	120
gcgacgcatg	cttgcgtgcc	tacggacccc	aacccccagg	aggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtcctt	gaagccctgc	gtgaagctga	cgctctcttg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgatg	tggccccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tcgcatcctt	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	caccagctg	720
ctgctgaacg	ggtccctggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtctgtgg	cgattaactg	taccggcctt	840
aacaacaaca	cccgttaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	ccgcgcgcca	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcgagga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggagag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcaccttc	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	ccccccatcg	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320
aacgagacgg	agatcttcag	gcccggcggc	ggcgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaagggtgg	gaagggtggag	ccgctcggcg	tggccccac	ccgggccaag	1440
cgccgcgtcg	tgcagagaa	gggtgcccga	gcttcggtac	tgtctggtgg	agagctggac	1500
agatggggaga	aaattaggct	gcgcccggga	ggcaaaaaga	aatacaagct	caagcatatc	1560
gtgtgggcct	cgaggagct	tgaacgggtt	gccgtgaacc	caggcctgct	ggaaacatct	1620
gagggatgtc	gccagatcct	ggggcaattg	cagccatccc	tccagaccgg	gagtgaagag	1680
ctgaggtcct	tgtataacac	agtggctacc	ctctactgcg	tacaccagag	gatcgagatt	1740
aaggatacca	aggaggcctt	ggacaaaatt	gaggaggagc	aaaacaagag	caagaagaag	1800
gcccagcagg	cagctgctga	cactgggcat	agcaaccagg	tatcacagaa	ctatcctatt	1860
gtccaaaaca	ttcaggggcca	gatggttcat	caggccatca	gcccccgac	gctcaatgcc	1920
tgggtgaagg	ttgtcgaaga	gaaggccttt	tctcctgagg	ttatcccat	gttctccgct	1980
ttgagtgaagg	gggccactcc	tcaggacctc	aatacaatgc	ttaataccgt	gggcggccat	2040
caggccgcca	tgcaaatgtt	gaaggagact	atcaacgagg	aggcagccga	gtgggacaga	2100
gtgcatcccg	tccacgctgg	cccaatcgcg	cccggacaga	tgcgggagcc	tcgcggtctt	2160
gacattgccc	gcaccacctc	tacactgcaa	gagcaaatcg	gatggatgac	caacaatcct	2220
cccatcccag	ttggagaaat	ctataaacgg	tggatcattc	tcggtctcaa	taaaattggt	2280
agaatgtact	ctccgacatc	catccttgac	attagacagg	gacccaaaga	gccttttagg	2340
gattacgtcg	accggtttta	taagaccctg	cgagcagagc	aggcctctca	ggaggtcaaa	2400
aactggatga	cggagacact	cctggtacag	aacgctaacc	ccgactgcaa	aacaatcttg	2460
aaggcactag	gcccggctgc	caccctggaa	gagatgatga	ccgcctgtca	gggagtaggc	2520
ggaccgggac	acaaagccag	agtgttgatg	ggcaagtggg	caaaaagtag	tgtggttgga	2580
tggcctactg	taagggaag	aatgagacga	gctgagccag	cagcagatgg	ggtgggagca	2640
gcattctcag	acctggaaaa	acatggagca	atcacaaagta	gcaatacagc	agctaccaat	2700
gctgcttggt	cctggctaga	agcacaagag	gaggaggagg	tgggttttcc	agtcacacct	2760
caggtacctt	taagaccaat	gacttacaag	gcagctgtag	atcttagcca	cttttttaaa	2820
gaaaaggggg	gactggaagg	gctaattcac	tcccaacgaa	gacaagatat	ccttgatctg	2880
tggatctacc	acacacaagg	ctacttccct	gattggcaga	actacacacc	agggccaggg	2940
gtcagatatc	cactgacctt	tggatggtgc	tacaagctag	taccagttga	gccagataag	3000
gtagaagagg	ccaataaagg	agagaacacc	agcgccttac	accctgtgag	cctgcatgga	3060
atggatgacc	ctgagagaga	agtgttagag	tggaggtttg	acagccgcct	agcatttcat	3120
cacgtggccc	gagagctgca	tccggagtag	ttcaagaact	gcactagtga	gccagtagat	3180
cctagactag	agccctggaa	gcattccagga	agtcagccta	aaactgcttg	taccaattgc	3240
tattgtaaaa	agtgttgctt	tcattgccaa	gtttgtttca	taacagctgc	cttaggcata	3300
tcctatggca	ggaagaagcg	gagacagcga	cgaagacctc	ctcaaggcag	tcagactcat	3360
caagtttctc	tatcaaagca	acccaccttc	caatccaaag	gggagccgac	aggcccgaag	3420
gaataa						3426

<210> 81

## seqlist.txt

<211> 1141  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 mL1-Nef Tatm fusion

<400> 81

Met	Ala	Glu	Gln	Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp
1				5					10					15	
Lys	Glu	Ala	Thr	Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr
			20					25					30		
Asp	Thr	Glu	Val	His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr
		35					40					45			
Asp	Pro	Asn	Pro	Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Tyr	Phe
	50					55					60				
Asn	Met	Trp	Lys	Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile
65				70					75					80	
Ser	Leu	Trp	Asp	Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu
			85					90						95	
Cys	Val	Thr	Leu	Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Asn	Ser	Thr	Thr
			100					105					110		
Thr	Thr	Ser	Asn	Gly	Trp	Thr	Gly	Glu	Ile	Arg	Lys	Gly	Glu	Ile	Lys
		115					120					125			
Asn	Cys	Ser	Phe	Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys
	130					135					140				
Glu	Tyr	Ala	Leu	Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp
145					150					155				160	
Asn	Ala	Thr	Thr	Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His
				165					170					175	
Cys	Asn	Ser	Ser	Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu
			180					185					190		
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys
		195					200					205			
Cys	Asn	Asn	Lys	Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser
	210					215					220				
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu
225					230					235					240
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp
			245					250						255	
Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser
			260					265					270		
Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile
		275					280					285			
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
	290					295					300				
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
305					310					315					320
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
			325						330				335		
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
			405						410					415	
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly
			420					425					430		
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465					470					475					480

## seqlist.txt

Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val
Leu	Met	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr	Val
Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly	Ala
Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn	Thr
Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu	Glu
Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr
Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly
Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu
Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys
Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu
Asn	Thr	Ser	Ala	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro

seqlist.txt

Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His  
 1025 1030 1035 1040  
 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser  
 1045 1050 1055  
 Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln  
 1060 1065 1070  
 Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His  
 1075 1080 1085  
 Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg  
 1090 1095 1100  
 Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His  
 1105 1110 1115 1120  
 Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro  
 1125 1130 1135  
 Thr Gly Pro Lys Glu  
 1140

<210> 82  
 <211> 3426  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 mL2-Nef Tatm fusion

<400> 82  
 atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60  
 accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgca taacgtgtgg 120  
 gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180  
 accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240  
 tctctgtggg accagtccct gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300  
 gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360  
 gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420  
 aaggtgcaga aggaatacgc gctgttttat aatctcgatg tggccccat cgacgacgac 480  
 aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540  
 gtcattgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600  
 cctgcccgat tcgcatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660  
 accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720  
 ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780  
 aacaccaaga caatcatcgt ccagctgaac gactctgtgg cgattaactg taccggcct 840  
 aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgccgc 900  
 aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960  
 accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020  
 aatcagagtt ctggcggaga ccccgagatc gtgcggcact ctttcaactg cgggggagc 1080  
 ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggaac 1140  
 aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200  
 tggcaggagg tgggaaaggc catgtatgcc cccccatcg ggggccagat ccgctgctcc 1260  
 tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320  
 aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380  
 ctgtacaagt acaagggtgt gaaggtggag ccgctcggcg tggccccac ccgggccaag 1440  
 cgccgcgtcg tgcagagaat ggggtgccga gcttcggtac tgtctggtgg agagctggac 1500  
 agatggggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560  
 gtgtggggcct cgaggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620  
 gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680  
 ctgaggtcct tgtataacac agtggctacc ctctactgcy tacaccagag gatcgagatt 1740  
 aaggatacca aggaggcctt ggacaaaatt gagggaggag aaaacaagag caagaagaag 1800  
 gcccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860  
 gtccaaaaca ttcagggcca gatggttcat caggccatca gccccggac gctcaatgcc 1920  
 tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatccccat gttctccgct 1980  
 ttgagtgagg gggccactcc tcaggacctc aatacaatgc ttaataaccgt gggcggccat 2040  
 caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100  
 gtgcatcccg tccacgctgg cccaatcgcy cccggacaga tgcgggagcc tcgcggtctc 2160  
 gacattgccg gcaccacctc tacactgcaa gagcaaactc gatggatgac caacaatcct 2220  
 cccatcccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattgtt 2280  
 agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340  
 gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400  
 aactggatga cgagagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460



seqlist.txt

```

aaggcactag gcccggctgc caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggaccccgac acaaagccag agtggtgatg ggcaagtggc caaaaagtag tgtggttgga 2580
tggcctactg taagggaag aatgagacga gctgagccag cagcagatgg ggtgggagca 2640
gcatctcgag acctggaaaa acatggagca atcacaagta gcaatacagc agctaccaat 2700
gctgcttggt cctggctaga agcacaagag gaggaggagg tgggttttcc agtcacacct 2760
caggtacctt taagaccaat gacttacaag gcagctgtag atcttagcca ctttttaaaa 2820
gaaaaggggg gactggaagg gctaattcac tcccaacgaa gacaagatat ccttgatctg 2880
tggatctacc acacacaagg ctacttccct gattggcaga actacacacc agggccaggg 2940
gtcagatatc cactgacctt tggatggtgc tacaagctag taccagttga gccagataag 3000
gtagaagagg ccaataaagg agagaacacc agcttggcac accctgtgag cctgcatgga 3060
atggatgacc ctgagagaga agtggttagag tggagggttg acagccgcct agcatttcat 3120
cacgtggccc gagagctgca tccggagtag ttcaagaact gcactagtga gccagtagat 3180
cctagactag agccctggaa gcatccagga agtcagccta aaactgcttg taccaattgc 3240
tattgtaaaa agtggttgctt tcattgccaa gtttggttca taacagctgc cttaggcatc 3300
tcctatggca ggaagaagcg gagacagcga cgaagacctc ctcaaggcag tcagactcat 3360
caagtttctc tatcaaagca acccacctcc caatccaaag gggagccgac agggccgaag 3420
gaataa

```

<210> 83

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mL2-Nef Tatm fusion

<400> 83

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100     105     110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115     120     125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130     135     140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145     150     155     160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165     170     175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180     185     190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195     200     205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210     215     220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225     230     235     240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245     250     255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260     265     270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275     280     285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290     295     300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305     310     315     320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys

```



## seqlist.txt

Thr	Ile	Lys	Phe	325 Asn	Gln	Ser	Ser	Gly	330 Gly	Asp	Pro	Glu	Ile	335 Val	Arg
His	Ser	Phe	340 Asn	Cys	Gly	Gly	Glu	345 Phe	Phe	Tyr	Cys	Asp	350 Thr	Thr	Gln
Leu	Phe	355 Asn	Ser	Thr	Trp	Asn	Gly	360 Thr	Glu	Gly	Asn	365 Asn	Thr	Glu	Gly
Asn	Ser	370 Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385 Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
Ile	Arg	Cys	340 Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465 Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
545 Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
625 Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
705 Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys
785 Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val
Leu	Met	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr	Val
Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly	Ala

seqlist.txt

865	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn	Thr
870																
885	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu	Glu
900																
915	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr
920																
935	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly
940																
955	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu
960																
975	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
980																
985	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys
990																
1005	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu
1010																
1015	Asn	Thr	Ser	Leu	Ala	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro
1020																
1035	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His
1040																
1055	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr	Ser
1060																
1065	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser	Gln
1070																
1085	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe	His
1090																
1095	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg
1100																
1110	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	His
1115																
1120	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Lys	Gly	Glu	Pro
1125																
1130	Thr	Gly	Pro	Lys	Glu											
1135																
1140																

<210> 84  
 <211> 4662  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c RT trNef p17/24 fusion

<400> 84

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaa	gcctacgaca	cggaagtgca	taacgtgtgg	120
gcgacgcatg	cttgctgtcc	tacggacccc	aacccccagg	aggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtccct	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgatg	tggtccccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgccggat	tcgcgatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	cacccagctg	720
ctgctgaacg	ggtccctggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtctgtgg	cgattaactg	taccgggcct	840
aacaacaaca	cccgttaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgcccc	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggagag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcaccctc	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	ccccccatcg	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320

seqlist.txt

```

aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcggag 1380
ctgtacaagt acaaggtggt gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat gggcccccac agtcccatcg agaccgtgcc ggtgaagctg 1500
aaacccggga tggacggccc caaggtcaag cagtggccac tcaccgagga gaagatcaag 1560
gccctggtgg agatctgcac cgagatggag aaagagggca agatcagcaa gatcgggcct 1620
gagaacccat acaacacccc cgtgtttgcc atcaagaaga aggacagcac caagtggcgc 1680
aagctggtgg atttccggga gctgaataag cggacccagg atttctggga ggtccagctg 1740
ggcatccccc atccggccgg cctgaagaag aagaagagcg tgaccgtgct ggacgtgggc 1800
gacgcttact tcagcgtccc tctggacgag gacttttagaa agtacaccgc ctttaccatc 1860
ccatctatca acaacgagac ccctggcatc agatatcagt acaacgtcct cccccagggc 1920
tggaagggct ctcccgccat tttccagagc tccatgacca agatcctgga gccgtttcgg 1980
aagcagaacc ccgatatcgt catctaccag tacatggacg acctgtacgt gggctctgac 2040
ctggaaatcg ggcagcatcg cacgaagatt gaggagctga ggcagcatct gctgagatgg 2100
ggcctgacca ctccggacaa gaagcatcag aaggagccgc cattcctgaa gatgggctac 2160
gagctccatc ccgacaagtg gaccgtgcag cctatcgtcc tccccgagaa ggacagctgg 2220
accgtgaacg acatccagaa gctggtgggc aagctcaact gggctagcca gatctatccc 2280
gggatcaagg tgcgccagct ctgcaagctg ctgcgcgga ccaaggccct gaccgaggtg 2340
attcccctca cggaggaagc cgagctcgag ctggctgaga accgggagat cctgaaggag 2400
cccgtgcacg gcgtgtacta tgaccctccc aaggacctga tcgccgaaat ccagaagcag 2460
ggccaggggc agtggacata ccagatttac caggagcctt tcaagaacct caagaccggc 2520
aagtacgccc gcatgagggg cgcccacacc aacgatgtca agcagctgac cgaggccgtc 2580
cagaagatca cgaccgagtc catcgtgatc tgggggaaga cacccaagtt caagctgcct 2640
atccagaagg agacctggga gacgtggtgg accgaatatt ggcaggccac ctggattccc 2700
gagtgggagt tcgtgaatac acctcctctg gtgaagctgt ggtaccagct cgagaaggag 2760
cccatcgtgg gcgcggagac attctacgtg gacggcgcgg ccaaccgcga aacaaagctc 2820
gggaaggccg ggtacgtcac caaccggggc cgccagaagg tcgtcaccct gaccgacacc 2880
accaaccaga agacggagct gcaggccatc tatctcgctc tccaggactc cggcctggag 2940
gtgaacatcg tgacggacag ccagtacgcg ctgggcatta ttcaggccca gccggaccag 3000
tccgagagcg aactggtgaa ccagattatc gagcagctga tcaagaaaga gaaggtctac 3060
ctcgcctggg tcccggccca taagggcatt ggcggcaacg agcaggtcga caagctggtg 3120
agtgcgggga ttagaaaggt gctgatggtg ggttttccag tcacacctca ggtaccttta 3180
agaccaatga cttacaaggc agctgtagat cttagccact ttttaaaga aaagggggga 3240
ctggaagggc taattcactc ccaaagaaga caagatatcc ttgatctgtg gatctaccac 3300
acacaaggct acttccctga ttggcagaac tacacaccag ggccaggggg cagatatcca 3360
ctgacctttg gatggtgcta caagctagta ccagttgagc cagataaggt agaagaggcc 3420
aataaaggag agaaccaccg cttgttacac cctgtgagcc tgcatgggat ggatgacccg 3480
gagagagaag tgttagagtg gaggtttgac agccgcctag catttcatca cgtggcccga 3540
gagctgcac cggagtactt caagaactgc atgggtgccc gagcttcggt actgtctggt 3600
ggagagctgg acagatggga gaaaattagg ctgcgcccgg gaggcaaaaa gaaatacaag 3660
ctcaagcata tcgtgtgggc ctcgaggag cttgaacggt ttgccgtgaa cccaggcctg 3720
ctggaacat ctgagggatg tcgccagatc ctggggcaat tgccagccat cctccagacc 3780
gggagtgaag agctgaggtc cttgtataac acagtggcta ccctctactg cgtacaccag 3840
aggatcgaga ttaaggatac caaggaggcc ttggacaaaa ttgaggagga gcaaaacaag 3900
agcaagaaga aggcccagca ggcagctgct gacactgggc atagcaacca ggtatcacag 3960
aactatccta ttgtccaaaa cattcagggc cagatggttc atcaggccat cagcccccg 4020
acgctcaatg cctgggtgaa ggttgtcgaa gagaaggcct tttctcctga ggttatcccc 4080
atgttctccg ctttgagtga gggggccact cctcaggacc tcaatacaat gcttaatacc 4140
gtgggcggcc atcaggccgc catgcaaatg ttgaaggaga ctatcaacga ggaggcagcc 4200
gagtgggaca gagtgcaccc cgtccacgct ggcccaatcg cgcccggaca gatgcgggag 4260
cctcgcggct ctgacattgc cggcaccacc tctacactgc aagagcaaat cggatggatg 4320
accaacaatc ctcccatccc agttggagaa atctataaac ggtggatcat cctgggcctg 4380
aacaagatcg tgcgcatgta ctctccgaca tccatccttg acattagaca gggaccctct 4440
gagcctttta gggattacgt cgaccggttt tataagacc tgcgagcaga gcaggcctct 4500
caggaggtca aaaactggat gacggagaca ctcctggtac agaacgctaa ccccgactgc 4560
aaaacaatct tgaaggcact aggcccggt gccaccctgg aagagatgat gaccgcctgt 4620
cagggagtag gcggacccgg acacaaagcc agagtgttgt aa 4662

```

<210> 85

<211> 1553

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c RT trNef p17/24 fusion

<400> 85

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp

1

5

10

15

## seqlist.txt

Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr  
 20 25 30  
 Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr  
 35 40 45  
 Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe  
 50 55 60  
 Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile  
 65 70 75 80  
 Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu  
 85 90 95  
 Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr  
 100 105 110  
 Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys  
 115 120 125  
 Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys  
 130 135 140  
 Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp  
 145 150 155 160  
 Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His  
 165 170 175  
 Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu  
 180 185 190  
 Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys  
 195 200 205  
 Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser  
 210 215 220  
 Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu  
 225 230 235 240  
 Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp  
 245 250 255  
 Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser  
 260 265 270  
 Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile  
 275 280 285  
 His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly  
 290 295 300  
 Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn  
 305 310 315 320  
 Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys  
 325 330 335  
 Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg  
 340 345 350  
 His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln  
 355 360 365  
 Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly  
 370 375 380  
 Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met  
 385 390 395 400  
 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln  
 405 410 415  
 Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly  
 420 425 430  
 Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro  
 435 440 445  
 Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr  
 450 455 460  
 Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys  
 465 470 475 480  
 Arg Arg Val Val Gln Arg Met Gly Pro Ile Ser Pro Ile Glu Thr Val  
 485 490 495  
 Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp  
 500 505 510  
 Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu  
 515 520 525  
 Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr  
 530 535 540  
 Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg  
 545 550 555 560



## seqlist.txt

Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp  
 565 570 575  
 Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys  
 580 585 590  
 Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu  
 595 600 605  
 Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn  
 610 615 620  
 Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly  
 625 630 635 640  
 Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu  
 645 650 655  
 Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met  
 660 665 670  
 Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr  
 675 680 685  
 Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr  
 690 695 700  
 Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Lys Met Gly Tyr  
 705 710 715 720  
 Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu  
 725 730 735  
 Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu  
 740 745 750  
 Asn Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys  
 755 760 765  
 Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile Pro Leu Thr  
 770 775 780  
 Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu  
 785 790 795 800  
 Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu  
 805 810 815  
 Ile Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu  
 820 825 830  
 Pro Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala  
 835 840 845  
 His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln Lys Ile Thr  
 850 855 860  
 Thr Glu Ser Ile Val Ile Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro  
 865 870 875 880  
 Ile Gln Lys Glu Thr Trp Glu Thr Trp Thr Glu Tyr Trp Gln Ala  
 885 890 895  
 Thr Trp Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys  
 900 905 910  
 Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val Gly Ala Glu Thr Phe  
 915 920 925  
 Tyr Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly  
 930 935 940  
 Tyr Val Thr Asn Arg Gly Arg Gln Lys Val Val Thr Leu Thr Asp Thr  
 945 950 955 960  
 Thr Asn Gln Lys Thr Glu Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp  
 965 970 975  
 Ser Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly  
 980 985 990  
 Ile Ile Gln Ala Gln Pro Asp Gln Ser Glu Ser Glu Leu Val Asn Gln  
 995 1000 1005  
 Ile Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu Ala Trp Val  
 1010 1015 1020  
 Pro Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp Lys Leu Val  
 1025 1030 1035 1040  
 Ser Ala Gly Ile Arg Lys Val Leu Met Val Gly Phe Pro Val Thr Pro  
 1045 1050 1055  
 Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp Leu Ser  
 1060 1065 1070  
 His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His Ser Gln  
 1075 1080 1085  
 Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr  
 1090 1095 1100



seqlist.txt

Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro  
 1105 1110 1115 1120  
 Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro Asp Lys  
 1125 1130 1135  
 Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His Pro Val  
 1140 1145 1150  
 Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu Trp Arg  
 1155 1160 1165  
 Phe Asp Ser Arg Leu Ala Phe His His Val Ala Arg Glu Leu His Pro  
 1170 1175 1180  
 Glu Tyr Phe Lys Asn Cys Met Gly Ala Arg Ala Ser Val Leu Ser Gly  
 1185 1190 1195 1200  
 Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys  
 1205 1210 1215  
 Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu  
 1220 1225 1230  
 Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg  
 1235 1240 1245  
 Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu  
 1250 1255 1260  
 Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln  
 1265 1270 1275 1280  
 Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu  
 1285 1290 1295  
 Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr  
 1300 1305 1310  
 Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile  
 1315 1320 1325  
 Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala  
 1330 1335 1340  
 Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro  
 1345 1350 1355 1360  
 Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr  
 1365 1370 1375  
 Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys  
 1380 1385 1390  
 Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val  
 1395 1400 1405  
 His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser  
 1410 1415 1420  
 Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Ile Gly Trp Met  
 1425 1430 1435 1440  
 Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile  
 1445 1450 1455  
 Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile  
 1460 1465 1470  
 Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp  
 1475 1480 1485  
 Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys  
 1490 1495 1500  
 Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys  
 1505 1510 1515 1520  
 Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met  
 1525 1530 1535  
 Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val  
 1540 1545 1550  
 Leu

<210> 86  
 <211> 4662  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 RT trNef p17/24 ds gp120c fusion

## seqlist.txt

&lt;400&gt; 86

atgggcccc	tcagtcccat	cgagaccgtg	ccggtgaagc	tgaaacccgg	gatggacggc	60
cccaaggtca	agcagtggcc	actcaccgag	gagaagatca	aggccctggg	ggagatctgc	120
accgagatgg	agaaagaggg	caagatcagc	aagatcgggc	cggagaaccc	atacaacacc	180
cccgtgtttg	ccatcaagaa	gaaggacagc	accaagtggc	gcaagctggg	ggattttccg	240
gagctgaata	agcggaccca	ggattttctg	gaggtccagc	tgggcatccc	ccatccggcc	300
ggcctgaaga	agaagaagag	cgtgaccgtg	ctggacgtgg	gcgacgctta	cttcagcgtc	360
cctctggacg	aggacttttag	aaagtacacc	gcctttacca	tcccatctat	caacaacgag	420
acccctggca	tcagatatca	gtacaacgct	ctcccccagg	gctggaaggg	ctctcccgcc	480
atttttccaga	gctccatgac	caagatcctg	gagccgtttc	ggaagcagaa	ccccgatatc	540
gtcatctacc	agtacatgga	cgacctgtac	gtgggctctg	acctggaaat	cgggcagcat	600
cgcacgaaga	ttgaggagct	gaggcagcat	ctgctgagat	ggggcctgac	cactccggac	660
aagaagcatc	agaaggagcc	gccattcctg	aagatgggct	acgagctcca	tcccgacaag	720
tggaccgtgc	agcctatcgt	cctccccgag	aaggacagct	ggaccgtgaa	cgacatccag	780
aagctgggtg	gcaagctcaa	ctgggctagc	cagatctatc	ccgggatcaa	ggtgcgccag	840
ctctgcaagc	tgctgcgcgg	caccaaggcc	ctgaccgagg	tgattccccct	cacggaggaa	900
gccgagctcg	agctggctga	gaaccgggag	atcctgaagg	agcccgtgca	cggcgtgtac	960
tatgaccctt	ccaaggacct	gatcgccgaa	atccagaagc	agggccaggg	gcagtggaca	1020
taccagattt	accaggagcc	tttcaagaac	ctcaagaccg	gcaagtacgc	ccgcatgagg	1080
ggcggccaca	ccaacgatgt	caagcagctg	accgaggccg	tccagaagat	cacgaccgag	1140
tccatcgtga	tctgggggaa	gacacccaag	ttcaagctgc	ctatccagaa	ggagacctgg	1200
gagacgtggg	ggaccgaata	ttggcaggcc	acctggattc	ccgagtggga	gttcgtgaat	1260
acacctcttc	tgggtgaagct	gtggtaccag	ctcgagaagg	agcccattcgt	gggcgcggag	1320
acattctacg	tggacggcgc	ggccaaccgc	gaaacaaagc	tcgggaaggc	cgggtacgtc	1380
accaaccggg	gccgccagaa	ggtcgtcacc	ctgaccgaca	ccaccaacca	gaagacggag	1440
ctgcaggcca	tctatctcgc	tctccaggac	tccggcctgg	aggtgaacat	cgtgacggac	1500
agccagtagc	cgctgggcat	tattcaggcc	cagccggacc	agtccgagag	cgaactgggtg	1560
aaccagatta	tcgagcagct	gatcaagaaa	gagaagggtc	acctcgccctg	ggtcccggcc	1620
cataagggca	ttggcggcaa	cgagcaggtc	gacaagctgg	tgagtgcggg	gattagaaag	1680
gtgctgatgg	tgggttttcc	agtcacacct	caggtacctt	taagaccaat	gacttacaag	1740
gcagctgtag	atcttagcca	cttttttaaaa	gaaaaggggg	gactggaagg	gctaattcac	1800
tcccaaagaa	gacaagatat	ccttgatctg	tggatctacc	acacacaagg	ctacttccct	1860
gattggcaga	actacacacc	agggccaggg	gtcagatatc	cactgacctt	tggatgggtg	1920
tacaagctag	taccagttga	gccagataag	gtagaagagg	ccaataaagg	agagaacacc	1980
agcttggttac	accctgtgag	cctgcatggg	atggatgacc	cggagagaga	agtgttagag	2040
tggagggtttg	acagccgcct	agcatttcat	cacgtggccc	gagagctgca	tccggagtac	2100
ttcaagaact	gcatgggtgc	ccgagcttcg	gtactgtctg	gtggagagct	ggacagatgg	2160
gagaaaatta	ggctgcgccc	gggaggcaaa	aagaaataca	agctcaagca	tatcgtgtgg	2220
gcctcgaggg	agcttgaacg	gtttgcccgtg	aaccagggcc	tgctggaaac	atctgaggga	2280
tgctcgccaga	tcctggggca	attgcagcca	tccctccaga	ccgggagtga	agagctgagg	2340
tccttgtata	acacagtggc	taccctctac	tgcgtacacc	agaggatcga	gattaaggat	2400
accaaggagg	ccttggacaa	aattgaggag	gagcaaaaaca	agagcaagaa	gaaggcccag	2460
caggcagctg	ctgacactgg	gcatagcaac	caggtatcac	agaactatcc	tattgtccaa	2520
aacattcagg	gccagatggg	tcatcaggcc	atcagccccc	ggacgctcaa	tgcctgggtg	2580
aaggttgtcg	aagagaaggc	ctttttctcct	gaggttatcc	ccatgtttctc	cgctttgagt	2640
gagggggcca	ctcctcagga	cctcaataca	atgcttaata	ccgtggggcg	ccatcaggcc	2700
gccatgcaaa	tgttgaagga	gactatcaac	gaggaggcag	ccgagtggga	cagagtgcac	2760
cccgtccacg	ctggcccaat	cgcgcccggg	cagatgcggg	agcctcgcg	ctctgacatt	2820
gccggcacca	cctctacact	gcaagagcaa	atcggatgga	tgaccaacaa	tcctcccatc	2880
ccagttggag	aaatctataa	acgggtggatc	atcctggggc	tgaacaagat	cgtgcgcatg	2940
tactctccga	catccatcct	tgacattaga	cagggaccca	aagagccttt	tagggattac	3000
gtcgaccggg	tttataagac	cctgcgagca	gagcaggcct	ctcaggagggt	caaaaactgg	3060
atgacggaga	cactcctggg	acagaacgct	aaccccagct	gcaaaaacaat	cttgaaggca	3120
ctaggcccgg	ctgccaccct	ggaagagatg	atgaccgcct	gtcaggggagt	aggcggaccc	3180
ggacacaaag	ccagagtgtt	gatggccgag	cagctgtggg	tcaccgtcta	ctacggcgtg	3240
cctgtgtgga	aggaggccac	gaccaccctc	ttctgcgcga	gcgacgcca	ggcctacgac	3300
acggaagtgc	ataacgtgtg	ggcgacgcat	gcttgcggtg	ctacggaccc	caaccccag	3360
gaggtggtgc	tgggaaacgt	gaccgagtac	ttcaacatgt	ggaagaataa	catggtggat	3420
cagatgcacg	aggacatcat	ctctctgtgg	gaccagtccc	tgaagccctg	cgtgaagctg	3480
acgcctctct	gcgtgacact	ggactgtgac	gacgtcaaca	ccaccaacag	cactaccacc	3540
accagcaacg	gctggaccgg	agagattcgg	aagggcgaga	tcaagaactg	ctccttcaat	3600
atcacgacct	cgatcagaga	caaggtgcag	aaggaatacg	cgctgtttta	taatctcgat	3660
gtggtcccca	tcgacgacga	caatgccacc	accaagaaca	agacgacgcg	taatttcaga	3720
ctcattcact	gcaacagcag	cgatcatgacg	caggcctgcc	ccaaggtgtc	cttcgaacca	3780
atcccgatcc	attactgtgc	ccctgccgga	ttcgcgatcc	tcaagtgtaa	caacaagacc	3840
ttcgacggga	agggcctgtg	caccaacgtc	agcacgggtg	agtgacacca	tggcatccgc	3900
cccgtcgtga	gcacccagct	gctgctgaac	gggtccctgg	ctgaggagga	ggtggtgatc	3960
cggctcgaca	acttcatgga	caacaccaag	acaatcatcg	tccagctgaa	cgagtctgtg	4020

## seqlist.txt

```

gcgattaact gtacccggcc taacaacaac acccgtaagg gcatccacat cgggcctgga 4080
cgggccttct atgccgcccg caagatcatc ggcgacatcc ggcaggccca ttgcaacctc 4140
tcccgcgccc agtgggaataa caccctgaag cagatcgtga tcaagctgag agagcacttt 4200
ggaaacaaga ccatcaagtt caatcagagt tctggcgagg accccgagat cgtgcggcac 4260
tccttcaact gcgggggcca gttcttctac tgcgatacga cacagctctt caactccacc 4320
tggaacggca ccgagggcaa caacacagag ggaaactcca ctatcaccct cccttgccgc 4380
atcaagcaga tcatcaacat gtggcaggag gtgggaaagg ccatgtatgc cccccccatc 4440
ggggggccaga tccgctgctc ctccaacatc accggcctgc tgctcaccag agacgggggc 4500
accgagggca acggcacgga gaacgagacg gagatcttca ggcccggcgg cggcgacatg 4560
agggataact ggcggagcga gctgtacaag tacaagggtg tgaagggtga gccgctcggc 4620
gtggccccc a cccgggcca gcgccgcgctc gtgcagagat ga 4662

```

&lt;210&gt; 87

&lt;211&gt; 1553

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 RT trNef p17/24 ds gp120c fusion

&lt;400&gt; 87

```

Met Gly Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro
1      5      10      15
Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
20      25      30
Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
35      40      45
Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
50      55      60
Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65      70      75      80
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
85      90      95
Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
100     105     110
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
115     120     125
Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
130     135     140
Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145     150     155     160
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
165     170     175
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
180     185     190
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
195     200     205
Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
210     215     220
Lys Glu Pro Pro Phe Leu Lys Met Gly Tyr Glu Leu His Pro Asp Lys
225     230     235     240
Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
245     250     255
Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
260     265     270
Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
275     280     285
Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290     295     300
Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305     310     315     320
Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
325     330     335
Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
340     345     350
Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
355     360     365
Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile

```

## seqlist.txt

	370					375				380					
Trp	Gly	Lys	Thr	Pro	Lys	Phe	Lys	Leu	Pro	Ile	Gln	Lys	Glu	Thr	Trp
385					390					395					400
Glu	Thr	Trp	Trp	Thr	Glu	Tyr	Trp	Gln	Ala	Thr	Trp	Ile	Pro	Glu	Trp
				405					410					415	
Glu	Phe	Val	Asn	Thr	Pro	Pro	Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu
			420					425					430		
Lys	Glu	Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr	Val	Asp	Gly	Ala	Ala
		435					440				445				
Asn	Arg	Glu	Thr	Lys	Leu	Gly	Lys	Ala	Gly	Tyr	Val	Thr	Asn	Arg	Gly
	450					455					460				
Arg	Gln	Lys	Val	Val	Thr	Leu	Thr	Asp	Thr	Thr	Asn	Gln	Lys	Thr	Glu
465					470					475					480
Leu	Gln	Ala	Ile	Tyr	Leu	Ala	Leu	Gln	Asp	Ser	Gly	Leu	Glu	Val	Asn
				485					490					495	
Ile	Val	Thr	Asp	Ser	Gln	Tyr	Ala	Leu	Gly	Ile	Ile	Gln	Ala	Gln	Pro
			500					505					510		
Asp	Gln	Ser	Glu	Ser	Glu	Leu	Val	Asn	Gln	Ile	Ile	Glu	Gln	Leu	Ile
		515					520					525			
Lys	Lys	Glu	Lys	Val	Tyr	Leu	Ala	Trp	Val	Pro	Ala	His	Lys	Gly	Ile
	530					535					540				
Gly	Gly	Asn	Glu	Gln	Val	Asp	Lys	Leu	Val	Ser	Ala	Gly	Ile	Arg	Lys
545					550					555					560
Val	Leu	Met	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro
				565					570					575	
Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys
			580				585						590		
Gly	Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu
		595					600					605			
Asp	Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn
	610					615					620				
Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys
625					630					635					640
Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys
				645					650					655	
Gly	Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp
			660					665					670		
Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala
		675					680					685			
Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys
	690					695					700				
Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	Gly	Glu	Leu	Asp	Arg	Trp
705					710					715					720
Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys	Leu	Lys
				725					730					735	
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
			740					745					750		
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
		755					760					765			
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
	770					775					780				
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
785					790					795					800
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Ser	Lys
				805					810					815	
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val
			820					825					830		
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
		835					840					845			
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
	850					855					860				
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
865					870					875					880
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
				885					890					895	
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
			900					905					910		
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala



## seqlist.txt

```

          915          920          925
Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
930
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
945
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
960
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
975
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
990
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
1005
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
1020
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
1040
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Ala Glu Gln Leu
1055
Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr
1070
Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His
1085
Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
1100
Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys Asn
1120
Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln
1135
Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asp
1150
Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn Gly
1165
Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
1180
Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu Phe
1200
Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asn Ala Thr Thr Lys
1215
Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser Val
1230
Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His
1245
Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr
1260
Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys Thr
1275
His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser
1290
Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp Asn
1305
Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn Cys
1320
Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro Gly
1335
Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln Ala
1350
His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln Ile
1365
Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe Asn
1380
Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn Cys
1395
Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser Thr
1410
Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile Thr
1425
Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly
1445

```



seqlist.txt

	1460		1465		1470
Lys	Ala	Met	Tyr	Ala	Pro
	1475		1480		1485
Asn	Ile	Thr	Gly	Leu	Leu
	1490		1495		1500
Gly	Thr	Glu	Asn	Glu	Thr
1505			1510		1515
Arg	Asp	Asn	Trp	Arg	Ser
	1525		1530		1535
Glu	Pro	Leu	Gly	Val	Ala
	1540		1545		1550
Arg					

<210> 88  
 <211> 3204  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 RT trNef p17/24 fusion

<400> 88

atgggccc	tcagtccc	cgagaccg	ccggtga	tgaaaccc	gatggacg	60
ccaagg	agcagt	actcaccg	gagaaga	aggccctg	ggagatct	120
accgag	agaaag	caagatca	aagatcgg	ctgagaac	atacaaac	180
cccggt	ccatcaa	gaaggaca	accaagt	gcaagctg	ggatttcc	240
gagctga	agcggacc	ggatttct	gaggtcc	tgggcatc	ccatccgg	300
ggcctga	agaaga	cgtgaccg	ctggacg	gcgacgct	cttcagcg	360
cctctgg	aggact	aaagta	gcctttac	tcccatct	caacaacg	420
accctgg	tcagata	gtacaacg	ctccccag	gctggaag	ctctcccg	480
attttcc	gctccat	caagatcc	gagccgtt	ggaagcag	ccccgata	540
gtcatct	agtacat	cgacctgt	gtgggctc	acctggaa	cgggcagc	600
cgcacga	ttgagg	gaggcagc	ctgctgag	ggggcctg	cactccgg	660
aagaagc	agaagg	gccattcc	aagatggg	acgagctc	tcccgaca	720
tggaccg	agcctat	cctccccg	aaggacag	ggaccgtg	cgacatcc	780
aagctgg	gcaagct	ctgggcta	cagatcta	ccgggatc	ggtgcgcc	840
ctctgca	tgctg	caccaagg	ctgaccga	tgattccc	cacggagg	900
gccgagc	agctggc	gaaccggg	atcctga	agcccgtg	cggcgtgt	960
tatgacc	ccaagg	gatcgccg	atccaga	agggccag	gcagtgg	1020
taccaga	accagg	tttcaaga	ctcaaga	gcaagtac	ccgcatga	1080
ggcgc	ccaacg	caagcagc	accgagg	tccagaag	cacgaccg	1140
tccatcg	tctggg	gacaccca	ttcaagc	ctatccag	ggagacct	1200
gagacgt	ggaccga	ttggcagg	acctggat	ccgagtgg	gttcgtga	1260
acacctc	tggtga	gtggtacc	ctcgaga	agcccatc	gggcgcgg	1320
acattct	tgga	ggccaacc	gaaacaa	tcgggaag	cgggtacg	1380
accaacc	gccgcc	ggtcgtca	ctgaccga	ccaccaac	gaagacgg	1440
ctgcagg	tctatct	tctccagg	tccggcct	aggtgaac	cgtgacgg	1500
agccagt	cgctggg	tattcagg	cagccgg	agtccgag	cgaactgg	1560
aaccaga	tcgagc	gatcaaga	gagaagg	acctcgcc	ggtcccgg	1620
cataagg	ttggcg	cgagcagg	gacaagc	tgagtgcg	gattagaa	1680
gtgctga	tggttt	agtcacac	caggtacc	taagacca	gacttaca	1740
gcagctg	atcttag	ctttttaa	gaaaagg	gactgga	gctaattc	1800
tcccaa	gacaaga	ccttgatc	tgatctac	acacaca	ctacttcc	1860
gattggc	actacac	agggccag	gtcagata	cactgacc	tggatgg	1920
tacaagc	taccagt	gccagata	gtagaaga	ccaataa	agagaac	1980
agcttgt	accctgt	cctgcatg	atggatga	cggagaga	agtgttag	2040
tggagg	acagccg	agcatttc	cacgtggc	gagagctg	tccggagt	2100
ttcaaga	gcatggg	ccgagctt	gtactgtc	gtggagag	ggacagat	2160
gagaaa	ggctgcg	gggaggca	aagaaata	agctcaag	tatcgtgt	2220
gcctcga	agcttga	gtttgccg	aacccagg	tgctggaa	atctgagg	2280
tgctcgc	tcctggg	attgcagc	tccctcca	ccgggagt	agagctga	2340
tccttgt	acacagt	taccctct	tgcgtacc	agaggatc	gattaagg	2400
accaagg	ccttgga	aattgagg	gagcaaaa	agagcaag	gaaggccc	2460
caggcag	ctgacac	gcatagca	caggtatc	agaactat	tattgtcc	2520
aacattc	gccagat	tcatcagg	atcagccc	ggacgcta	tgcctggg	2580
aaggttg	aagaga	cttttctc	gaggttat	ccatgttc	cgctttga	2640

## seqlist.txt

```

gaggggggcca ctcctcagga cctcaataca atgcttaata ccgtgggcg ccatcaggcc 2700
gccatgcaaa tgttgaagga gactatcaac gaggaggcag ccgagtggga cagagtgcatt 2760
cccgtccacg ctggcccaat cgcgcccga cagatgcggg agcctcgcgg ctctgacatt 2820
gccggcacca cctctacact gcaagagcaa atcggatgga tgaccaacaa tcctcccatc 2880
ccagttggag aaatctataa acggtggatc atcctgggccc tgaacaagat cgtgcgcatg 2940
tactctccga catccatcct tgacattaga cagggaccca aagagccttt tagggattac 3000
gtcgaccggt tttataagac cctgcgagca gagcaggcct ctcaggagggt caaaaactgg 3060
atgacggaga cactcctggg acagaacgct aaccccgact gcaaaaacaat cttgaaggca 3120
ctaggcccgg ctgccaccct ggaagagatg atgaccgcct gtcaggaggat aggcggaccc 3180
ggacacaaag ccagagtgtt gtaa 3204

```

&lt;210&gt; 89

&lt;211&gt; 1067

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 RT trNef p17/24 fusion

&lt;400&gt; 89

```

Met Gly Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro
1      5      10      15
Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
20      25      30
Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
35      40      45
Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
50      55      60
Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65      70      75      80
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
85      90      95
Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
100     105     110
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
115     120     125
Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
130     135     140
Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145     150     155     160
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
165     170     175
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
180     185     190
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
195     200     205
Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
210     215     220
Lys Glu Pro Pro Phe Leu Lys Met Gly Tyr Glu Leu His Pro Asp Lys
225     230     235     240
Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
245     250     255
Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
260     265     270
Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
275     280     285
Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290     295     300
Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305     310     315     320
Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
325     330     335
Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
340     345     350
Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
355     360     365
Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
370     375     380

```

## seqlist.txt

Trp 385	Gly	Lys	Thr	Pro	Lys 390	Phe	Lys	Leu	Pro	Ile 395	Gln	Lys	Glu	Thr	Trp 400
Glu	Thr	Trp	Trp	Thr 405	Glu	Tyr	Trp	Gln	Ala 410	Thr	Trp	Ile	Pro	Glu 415	Trp
Glu	Phe	Val	Asn 420	Thr	Pro	Pro	Leu	Val 425	Lys	Leu	Trp	Tyr	Gln 430	Leu	Glu
Lys	Glu	Pro 435	Ile	Val	Gly	Ala	Glu 440	Thr	Phe	Tyr	Val	Asp 445	Gly	Ala	Ala
Asn 450	Arg	Glu	Thr	Lys	Leu	Gly 455	Lys	Ala	Gly	Tyr	Val 460	Thr	Asn	Arg	Gly
Arg 465	Gln	Lys	Val	Val	Thr 470	Leu	Thr	Asp	Thr	Thr 475	Asn	Gln	Lys	Thr	Glu 480
Leu	Gln	Ala	Ile	Tyr 485	Leu	Ala	Leu	Gln	Asp 490	Ser	Gly	Leu	Glu	Val 495	Asn
Ile	Val	Thr	Asp 500	Ser	Gln	Tyr	Ala	Leu 505	Gly	Ile	Ile	Gln	Ala 510	Gln	Pro
Asp	Gln	Ser 515	Glu	Ser	Glu	Leu	Val 520	Asn	Gln	Ile	Ile	Glu 525	Gln	Leu	Ile
Lys	Lys 530	Glu	Lys	Val	Tyr	Leu 535	Ala	Trp	Val	Pro	Ala 540	His	Lys	Gly	Ile
Gly 545	Gly	Asn	Glu	Gln	Val 550	Asp	Lys	Leu	Val	Ser 555	Ala	Gly	Ile	Arg	Lys 560
Val	Leu	Met	Val	Gly 565	Phe	Pro	Val	Thr	Pro 570	Gln	Val	Pro	Leu	Arg 575	Pro
Met	Thr	Tyr	Lys 580	Ala	Ala	Val	Asp	Leu 585	Ser	His	Phe	Leu	Lys 590	Glu	Lys
Gly	Gly	Leu 595	Glu	Gly	Leu	Ile	His 600	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu
Asp	Leu 610	Trp	Ile	Tyr	His	Thr 615	Gln	Gly	Tyr	Phe	Pro 620	Asp	Trp	Gln	Asn
Tyr 625	Thr	Pro	Gly	Pro	Gly 630	Val	Arg	Tyr	Pro	Leu 635	Thr	Phe	Gly	Trp	Cys 640
Tyr	Lys	Leu	Val	Pro 645	Val	Glu	Pro	Asp	Lys 650	Val	Glu	Glu	Ala	Asn 655	Lys
Gly	Glu	Asn	Thr 660	Ser	Leu	Leu	His	Pro 665	Val	Ser	Leu	His	Gly 670	Met	Asp
Asp	Pro	Glu 675	Arg	Glu	Val	Leu	Glu 680	Trp	Arg	Phe	Asp	Ser 685	Arg	Leu	Ala
Phe	His 690	His	Val	Ala	Arg	Glu 695	Leu	His	Pro	Glu	Tyr 700	Phe	Lys	Asn	Cys
Met 705	Gly	Ala	Arg	Ala	Ser 710	Val	Leu	Ser	Gly	Gly 715	Glu	Leu	Asp	Arg	Trp 720
Glu	Lys	Ile	Arg	Leu 725	Arg	Pro	Gly	Gly	Lys 730	Lys	Lys	Tyr	Lys	Leu 735	Lys
His	Ile	Val	Trp 740	Ala	Ser	Arg	Glu	Leu 745	Glu	Arg	Phe	Ala	Val 750	Asn	Pro
Gly	Leu	Leu 755	Glu	Thr	Ser	Glu	Gly 760	Cys	Arg	Gln	Ile	Leu 765	Gly	Gln	Leu
Gln	Pro 770	Ser	Leu	Gln	Thr	Gly 775	Ser	Glu	Glu	Leu	Arg 780	Ser	Leu	Tyr	Asn
Thr 785	Val	Ala	Thr	Leu	Tyr 790	Cys	Val	His	Gln	Arg 795	Ile	Glu	Ile	Lys	Asp 800
Thr	Lys	Glu	Ala	Leu 805	Asp	Lys	Ile	Glu	Glu 810	Glu	Gln	Asn	Lys	Ser 815	Lys
Lys	Lys	Ala	Gln 820	Gln	Ala	Ala	Ala	Asp 825	Thr	Gly	His	Ser	Asn 830	Gln	Val
Ser	Gln	Asn 835	Tyr	Pro	Ile	Val	Gln 840	Asn	Ile	Gln	Gly	Gln 845	Met	Val	His
Gln	Ala 850	Ile	Ser	Pro	Arg	Thr 855	Leu	Asn	Ala	Trp	Val 860	Lys	Val	Val	Glu
Glu 865	Lys	Ala	Phe	Ser	Pro 870	Glu	Val	Ile	Pro	Met 875	Phe	Ser	Ala	Leu	Ser 880
Glu	Gly	Ala	Thr	Pro 885	Gln	Asp	Leu	Asn	Thr 890	Met	Leu	Asn	Thr	Val 895	Gly
Gly	His	Gln	Ala 900	Ala	Met	Gln	Met	Leu 905	Lys	Glu	Thr	Ile	Asn 910	Glu	Glu
Ala	Ala	Glu 915	Trp	Asp	Arg	Val	His 920	Pro	Val	His	Ala	Gly 925	Pro	Ile	Ala

```

seqlist.txt
Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
930 935 940
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
945 950 955 960
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
965 970 975
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
980 985 990
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
995 1000 1005
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
1010 1015 1020
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
1025 1030 1035 1040
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
1045 1050 1055
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu
1060 1065

```